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Run
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Listing first 45 summaries
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                                                                                                                                                                                                                                                                       No.
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and is derived
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117.6
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Match
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Gapop 10.0 , Gapext 1.0
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(without alignments)
11109.172 Million cell updates/sec
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l: /cgn2_6/ptodata/1/pu
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Copyright (c) 1993 - 2005
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/ Cgn2_6/ptodata/1/pubpna/US08_PUBCOMB.seq:*
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/cgn2_6/ptodata/1/pubpna/USO6_PUBCOMB.seq:*
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688
2048
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US-10-032-585-6675
US-10-128-714-7563
US-10-128-714-7563
US-09-864-408A-2265
US-10-473-128-386
US-10-633-047-7103
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                                                              Sequence 6575, Ap
Sequence 2563, Ap
Sequence 7563, Ap
Sequence 2265, Ap
Sequence 386, App
Sequence 3103, Ap
Sequence 1563, Ap
Sequence 6563, Ap
                                         Sequence
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## ALIGNMENTS

Ś 밁 US-10-032-585-6675
; Sequence 6675, Application US/10032585
; Publication No. US20030180953A1
; GENERAL INFORMATION: 밁 S US-10-032-585-6675 NUMBER OF SEQ ID NOS: 8000 SOFTWARE: PatentIn version 3.1 SEQ ID NO 6675 LENGTH: 2769 Query Match 78.6%; Score 2769; Best Local Similarity 100.0%; Pred. No. 0; Matches 2769; Conservative 0; Mismatches APPLICANT: Terry, Roemer D.
APPLICANT: Bo, Jiang
APPLICANT: Charles, Boone
APPLICANT: Howard, Bussey
TITLE OF INVENTION: Gene Disruption Methodologies for Drug Target Discovery
FILE REFERENCE: 10182-005-999
CURRENT APPLICATION NUMBER: US/10/032,585
CURRENT FILING DATE: 2001-12-20 TYPE: DNA ORGANISM: Candida albicans 338 458 GAAGATGAGTTGGAATTAAAATCAGAATTAGAATCAGAAGTTGTAAAAAAGCGAAAAACAA 517 398 GATGAAGTATTGGATGATCATAGAAATCAAATCACTAATGATTGTGCCATTAGTGATAGT 457 61 ATGTCCGATAGTGAAAGTTATTATCAAAATTCAACTACTAATCAACCTATTCCTAGATCT ATGTCCGATAGTGAAAGTTATTATCAAAATTCAACTACTAATCAACCTATTCCTAGATCT 397 GATGAAGTATTGGATGATCATAGAAATCAAATCACTAATGATTGTGCCATTAGTGATAGT 120 Mismatches DB 16; <u>,</u> Length 2769; Indels 0, Gaps. 60

Sequence

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1538 CAATTATCATTAACTTCATCTACATCTTCTGCATCTGGATCTGGGTGGAAA 1597	1478 TCTTCAGAAGAATTTATGAATTGAAGACTAAACAACCACCTTACAAATATGATGAT 1537	1418 CCAAAAAATATTTTAAAGAAAACATTATCAAGATTTGAATTTACTCATGAAAAATTCTTCA 1477	1358 AATAAAAAAAATAATGGTGGTGGTGGTGGTGGTTGTATGGCAGCATTAAAATATACT 1417	1298 TCCAAAAATAATACTACTAGTGGTGCATCTCGTCATCCATATCATCACAGTAATAAT 1357	1238 TATTTACAAAAACAAATGATTGCTAAAAATATTCTGCGTATTGATGAATTTCAAAATCTT 1297	1178 GTTAATGGAATTGATGTGAAATTGATGAAATTTATTAGAGAAGA	1118 AGATCATCTCAAGAAACTGAAGAAGATGTTTGTTTTCCTATGGTTGGT	1058 GCTGCTGGTAGAAGACCATCTCGTTCATCTATTGATAGTGAAGCTGATTCTCATGCATCA 1117	998 ATTGGTGCTACAACCCTTGGTGTTGGAACTGGTACTACCGCCACTGCCACTGCCACTGCCACTGCT 1057	938 ACTAATGATAGTGAAGATATTACTAATACTAGCACCACTGCTAATCATATGAAACTTGGT 997	878 GGTCGTAATAATTCTAATAATTTTGAAAATGATTTAGTTAG	818 AAATCAAGAAAAATCTCAATTGGAAAAATTTACCTCCATTAATTA	758 ACTCATCTTGCAATTCCAATTCCAATTCCAACCCCAATTATTACTAATGCTAAT 817	698 TCATTACGTAAAGATTTTTATTTAAAAGATAATACTGACGACAATTCTACTAATAATCAT 757	638 TTATCTGGTGGTGATGATACTATTAACAGCGGTCACAAAAATCGTAATTATAACATGAGT 697	578 TCTTCAATTAAGAAAAATCTAATCTTACCGATAAAGATAGAATTACCAACCCTATGAGT 637	518 CAACAACATCATCAAGAGATTACATCAGATAATGCTAAACCATTGACTCGTAAATCTGGT 577	
9 5	P 5	₹ B £	\$ B &	\$ B &	B 8	8 8 8	8 8 8	, B <b>2</b>	\$ B &	5 B 8	}	P &	₹ # £	₹ ₩ 5	₹ B .	& B :	δ <u>β</u>	& B
2618 AGAGCTGATATTGCATTATATTTAGGTGATATTCAAGATCATCATATATACACCATGTTTCAA 20//	CARCARCACACACA SULTA CALLACACACACACACACACACACACACACACACACAC				GCTAATTCTTCTTCTGGTTATTATCAACGTCAATATAACTTACAACAACAACAACAACAACAACAACAA			CATGGAATTGAAGCTGATGCCATTGAAGATGCCGTTTTCACTGCTAGAGATACT		CICALICANCANA ISI AMAMSANANG I COLOMA I SHOMARI ARISI COMA SI ARISI CANTONI COMA SI ARISI CANTONI COMA SI ARISI COMA SI ARISI COMA SI ARISI COMA SI ARISI CANTONI		TATTTTGTTTGTTTCCATACTTTTGAAGCTGATAAAGAATCTGAAGATTATTTAGAACCG	TATTTTGTTTGTTTCCATACTTTTGAAGCTGATAAAGAATCTGAAGATTATTTAGAACCG				1658 CTTTTCCATTCTGAATCAGAAGAAACTATTCATGCCCCCGATATTCCATTAGTTATCA 1320	1201 CAATTATCATTAACTTCATCTACATCTTCTACTTCTGGATCTGGATCTGGGCAGGTGAAA 1260

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PRIOR APPLICATION NUMBER: US 60/316,362
PRIOR FILLING DATE: 2001-08-31
NUMBER OF SEQ ID NOS: 8603
SOFTWARE: PatentIn version 3.1
SEQ ID NO 2563
LENGTH: 1992
TYPE: DNA
ORGANISM: Aspergillus fumigatus
US-10-128-714-2563
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US-10-128-714-2563
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                              Query Match
Best Local Similarity
Matches 376; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 2563, Application US/10128714 Publication No. US20030119013A1
                                                                                                                                                                                                                                                                                       APPLICANT: Lemieux, Sebastien M
APPLICANT: Lemieux, Sebastien M
TITLE OF INVENTION: Methods of Use
TITLE OF INVENTION: MUMBER: US/10/128,714
CURRENT ETLING DATE: 2002-04-23
PRIOR APPLICATION NUMBER: US 60/285,697
PRIOR FILING DATE: 2001-04-23
PRIOR APPLICATION NUMBER: US 60/287,066
PRIOR FILING DATE: 2001-04-27
PRIOR APPLICATION NUMBER: US 60/285,890
PRIOR APPLICATION NUMBER: US 60/295,890
PRIOR APPLICATION NUMBER: US 60/303,899
PRIOR APPLICATION NUMBER: US 60/303,899
PRIOR FILING DATE: 2001-07-09
PRIOR FILING DATE: 2001-07-09
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APPLICANT: Hu, We
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1659 TTTTCCATTCTGAATCAGAAGAAACTATTCATGCCCCCGATATTCCATCATTAGTATCAC 1718
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Tishkoff, Daniel
Zamudio, Carlos
                                       Conservative
                                                         56.6%;
                                    0,
                                                       Score 179.6; DB 15;
Pred. No. 3e-20;
                                    Mismatches
                                  279;
                                       Indels
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                                                 APPLICANT: Hu, Wenqi
APPLICANT: Tishkoff, Daniel
APPLICANT: Zamudio, Carlos
APPLICANT: Zamudio, Carlos
APPLICANT: Eroshkin, Alexey M
APPLICANT: Lemieux, Sebastien M
TITLE OF INVENTION: Identification of Essential Genes in Aspergillus fumigatus and
TITLE OF INVENTION: Methods of Use
FILE REFERENCE: 10182-018-999
FILE REFERENCE: 10182-018-999
CURRENT APPLICATION NUMBER: US/10/128,714
CURRENT FILING DATE: 2002-04-23
FRIOR APPLICATION NUMBER: US 60/285,697
PRIOR APPLICATION NUMBER: US 60/287,066
PRIOR FILING DATE: 2001-04-23
PRIOR APPLICATION NUMBER: US 60/287,066
PRIOR APPLICATION NUMBER: US 60/287,066
PRIOR APPLICATION NUMBER: US 60/295,890
PRIOR APPLICATION NUMBER: US 60/295,890
PRIOR APPLICATION NUMBER: US 60/295,890
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APPLICANT: Hu, Wer
APPLICANT: Tishkor
APPLICANT: Zamudio
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Publication No. US20030119013A1
                                                                                                                                                                                                                                                                                                                                                                                               GENERAL INFORMATION:
                APPLICATION NUMBER: US 60/303,899 FILING DATE: 2001-07-09
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1499
  APPLICATION NUMBER: US 60/316,362
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; PRIOR FILING DATE: 2001-08-31
; NUMBER OF SEQ ID NOS: 8603
; SOFTWARE: PATEENTIN VERSION 3.1
; SEQ ID NO 7563
; LENGTH: 1992
; TYPE: DNA
; ORGANISM: Aspergillus fumigatu
US-10-128-714-7563
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                                                                                             GENERAL INFORMATION:
                                                                                                            Sequence 2265, Application US/09864408A Publication No. US20040009474A1
APPLICANT: Leach, Martin D.
APPLICANT: Shimkets, Richard A.
TITLE OF INVENTION: NO. US20040009474A1el Human
FILE REFERENCE 21402-012
CURRENT APPLICATION NUMBER: US/09/864,408A
CURRENT FILING DATE: 2001-05-24
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Pred. No. 3e-20;
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; PRIOR APPLICATION NUMBER: 60/206,690
; PRIOR FILING DATE: 2000-05-24
; NUMBER OF SEQ ID NOS: 9068
; SOFTWARE: FastSEQ for Windows Version 4.
; SEQ ID NO 2265
; LENGTH: 462
; TYPE: DNA
; ORGANISM: Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                          FILE REFERENCE:
CURRENT APPLICATION NUMBER: US/10/473,126
CURRENT FILING DATE: 2003-09-26
NUMBER OF SEQ ID NOS: 1258
SEQ ID NO 386
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GENERAL INFORMATION:
APPLICANT: Epigenomics AG
TITLE OF INVENTION: Methods and nucleic acids
TITLE OF INVENTION: proliferative disorders
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 386, Application US/10473126 Publication No. US20040234973A1
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Best Local
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Best Local Similarity 42.2%;
                                                                                                                                                                                                                                     Matches 1426; Conservative
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                                                                                                                                                                                                                                                                                                              OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)
                                                                                                                                                                                                                                                                                                                                                               TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                             LENGTH: 8056
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sal Similarity 67.5%;
166; Conservative
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TGAĀAGTTATTATCAAAATTCAACTAATCAACCTATTCCTAGATCTGATGAAGTATT
                                                TTAATATTAAGATNTTCCATTTTTTTTTTTTACCCAAGCTATGAAAATTATTTTTTGTTGT
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Pred. No. 1.4e-09;
0; Mismatches 1911;
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Pred. No. 3.7e-10;
0; Mismatches 80;
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                                       GAAAATAAATTAATGTTTAT 4768
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Sequence 7103, Application US/10653047 Publication No. US20040229367A1

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APPLICANT: Peter Bjarke Olsen
TITLE OF INVENTION: Methods For Monitoring Multiple Gen
TITLE DE INVENTION: Expression
FILE REFERENCE: 5849.200-US
CURRENT FAPPLICATION NUMBER: US/10/653,047
CURRENT FILING DATE: 2003-08-29
PRIOR APPLICATION NUMBER: US/09/533,559
PRIOR FILING DATE: 2000-03-22
PRIOR APPLICATION NUMBER: US/09/533,623
PRIOR FILING DATE: 1999-03-22
PRIOR PILING DATE: 1999-03-22
NUMBER OF SEQ ID NOS: 7860
SOFTWARE: FRASESEQ for Windows Version 4.0
SEQ ID NO 7103
LENGTH: 688
APPLICANT: Hau, Wengi
APPLICANT: Hau, Wengi
APPLICANT: Tishkoff, Daniel
APPLICANT: Tishkoff, Daniel
APPLICANT: Tishkoff, Carlos
APPLICANT: Zamudio, Carlos
APPLICANT: Lemieux, Sebastien M
APPLICANT: Lemieux, Sebastien M
TITLE OF INVENTION: Methods of Use
FILE REFERENCE: 10.182-018-999
CURRENT APPLICATION UMBER: US/10/128,714
CURRENT FILING DATE: 2002-04-23
PRIOR APPLICATION NUMBER: US 60/285,697
PRIOR FILING DATE: 2001-04-23
PRIOR FILING DATE: 2001-04-23
PRIOR FILING DATE: 2001-04-23
PRIOR FILING DATE: 2001-04-27
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; ORGANISM: Aspergillus oryzae
US-10-653-047-7103
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US-10-128-714-1563
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APPLICANT: Mandy M. Berka
APPLICANT: Michael W. Rey
APPLICANT: Jeffrey R.Shuster
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ilarity 61.6%;
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Pred. No. 8.1e-10;
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RESULT 8
US-10-128-714-6563
US-10-128-714-6563; Sequence 6563, Application US/10128714; Publication No. US20030119013A1; GENERAL INFORMATION:
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SEQ ID NO 1563
LENGTH: 2048
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PRIOR FILING DATE: 2001-08-31
NUMBER OF SEQ ID NOS: 8603
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; ORGANISM: Aspergillus fumigatus
US-10-128-714-6563
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Best Local Sim:
Matches 376;
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SEQ ID NO 6563
LENGTH: 2048
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APPLICANT: Eroshkin, Alexey M
APPLICANT: Lemieux, Sebastian M
TITLE OF INVENTION: Identification of Essential Genes in Aspergillus fumigatus and
TITLE OF INVENTION: Methods of Use
FILE REFERENCE: 10182-018-999
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PRIOR FILING DATE: 2001-04-23
PRIOR APPLICATION NUMBER: US 60/287,066
PRIOR FILING DATE: 2001-04-27
PRIOR APPLICATION NUMBER: US 60/295,890
PRIOR FILING DATE: 2001-06-05
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CURRENT FILING DATE: 2002-04-23
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FILING DATE: 2001-07-09
APPLICATION NUMBER: US 60/316,362
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Pred. No. 3.7e-09;
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; ORGANISM: Aspergillus
US-10-128-714-563
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Best Local Similarity
Matches 376; Conserv
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CURRENT APPLICATION NUMBER: US/10/128,714
CURRENT FILING DATE: 2002-04-23
PRIOR APPLICATION NUMBER: US 60/285,697
PRIOR FILING DATE: 2001-04-23
PRIOR APPLICATION NUMBER: US 60/287,066
PRIOR FILING DATE: 2001-04-27
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PRIOR FILING DATE: 2001-06-05
PRIOR APPLICATION NUMBER: US 60/303,899
PRIOR FILING DATE: 2001-07-09
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APPLICANT: Tishkoff, Daniel
APPLICANT: Zamudio, Carlos
APPLICANT: Eroshkin, Alexey M
APPLICANT: Lemieux, Sebastien M
TITLE OF INVENTION: Identification of
TITLE OF INVENTION: Methods of Use
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APPLICANT: Hu, W
APPLICANT: Tishk
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                                                                   TGGAGCCCGTCAACTTCTACATGGTTGTTTTCCGCGACGGTGTCCTCTCATTCTCATTCA
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Pred. No. 4.9e-
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APPLICANT: Hu, Wenqi
APPLICANT: Hu, Wenqi
APPLICANT: Tishkoff, Daniel
APPLICANT: Tishkoff, Daniel
APPLICANT: Exomidio, Carlos
APPLICANT: Exomidio, Carlos
APPLICANT: Ecoshkin, Alexey M
APPLICANT: Lemieux, Sebastien M
APPLICANT: Lemieux, Sebastien M
APPLICANT: Lemieux, Sebastien M
APPLICANT: Lemieux, Sebastien M
APPLICANTION: Methods of Use
FILE REFERENCE: 10182-018-999
CURRENT APPLICATION NUMBER: US/10/128,714
CURRENT APPLICATION NUMBER: US 60/285,697
PRIOR APPLICATION NUMBER: US 60/287,066
PRIOR FILING DATE: 2001-04-23
PRIOR APPLICATION NUMBER: US 60/287,066
PRIOR FILING DATE: 2001-04-27
PRIOR APPLICATION NUMBER: US 60/295,890
PRIOR APPLICATION NUMBER: US 60/303,899
PRIOR FILING DATE: 2001-07-09
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; ORGANISM: Aspergillus fumigatus
US-10-128-714-5563
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US-10-128-714-5563
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Best Local Sin
Matches 376;
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LENGTH: 4048
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 5563, Application US/10128714
Publication No. US20030119013A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NUMBER OF SEQ ID NOS: 8603
SOFTWARE: PatentIn version ? 1
EQ ID NO SEC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRIOR APPLICATION NUMBER: US 60/316,362
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CTTTAACTGCTGAAGATATTCGAATGCAAGAAACTCGTGAAAAAGTTGAATTATTTAAAA 1892
                                                                                                                                   TTTTCTCATCCGAGTCCCAGAGCACTGTGCATGCGGCGAACTGGGGGGACCTTGTGCTCC
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                                              ATTGTACTTGTCCTACTGATTCGGAAATGAAAATGTTGGCCAAAGCATTTGGTATTCATC
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Pred. No. 4.9e-09;
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RESULT 11
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                                                                                                                                                                                                                                    ; LENGTH: 4985
; TYPE: DNA
; ORGANIZM: Anopheles gambiae
US-10-094-240-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 10, Application US/10094240 Publication No. US20030082637A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                              PRIOR APPLICATION NUMBER: 60/264,649
PRIOR FILING DATE: 2001-01-26
NUMBER OF SEQ ID NOS: 27
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 10
                                                                                                                                                                            Matches
                                                                                                                                                                                                        Query Match
                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: ZWIEBEL, LAURENCE J.

TITLE OF INVENTION: ARRESTIN GENE, POLYPEPTIDE, AND METHODS OF USE THEREOF FILE REFERENCE: N8289

CURRENT APPLICATION NUMBER: US/10/094,240

CURRENT FILING DATE: 2001-03-08

PRIOR APPLICATION NUMBER: 10/056,405

PRIOR FILING DATE: 2002-01-24
                                                                                                                                                                                            Local Similarity
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                          AGTTGGAATTAAAATCAGAATTAGAATCAGAAGTTGTAAAAAGCGAAAAACAACAACAAC
                                                         ATAAGAACAACAACAACAATAATAAGAATAATAATAATAACAATAGCAATAATAAGA
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49.5%;
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                                                                                                                                                                                          Score 106.8; DB 14; Pred. No. 7.4e-08;
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                                                                                                                                                                                                                        ; TYPE: DNA
; ORGANISM: Anopheles gambiae
US-10-056-405-10
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US-10-056-405-10/c
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                                                                                                                                                                                          Query Match
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                                                                                                                                                                                                                                                                   LENGTH: 4985
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milarity 49.5%;
Conservative
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Sequence 10, Application US/10056405
Publication No. US20030166013A1
GENERAL INFORMATION:
APPLICANT: ZWIEBEL, LAURENCE J.
TITLE OF INVENTION: MOSQUITO OLFACTORY GENES, POLYPEPTIDES, AND METHODS
TITLE OF INVENTION: USE THEREOF
                                                                                                                                                                                                                                                                                                                                                                                                                                                 CURRENT APPLICATION NUMBER: US/10/056,405
CURRENT FILING DATE: 2002-01-24
PRIOR APPLICATION NUMBER: 60/264,649
PRIOR FILING DATE: 2001-01-26
NUMBER OF SEQ ID NOS: 23
                                                                3017 ATAAGAACAACAACAACAATAATAAGAATAATAATAATAACAATAGCAATAATAAGA 2958
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  345 ATAGTGAAAGTTATTATCAAAATTCAACTACTAATCAACCTATTCCTAGATCTGATGAAG
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ORGANISM: Pusarium venenatum; FEATURE; NAME/KEY: misc_feature; LOCATION: (1)...(575)
OTHER INFORMATION: n = A,T,C o: US-10-653-047-447
                                                                                                                                                                                             APPLICANT: Peter Bjarke Olsen
TITLE OF INVENTION: Methods For Monitoring Multiple Ger
TITLE OF INVENTION: Expression
FILE REFERENCE: 5849_200-US
CURRENT APPLICATION NUMBER: US/10/653,047
CURRENT FILING DATE: 2003-08-29
PRIOR APPLICATION NUMBER: US/09/533,559
PRIOR PILING DATE: 2000-03-22
PRIOR APPLICATION NUMBER: US/09/533,623
PRIOR APPLICATION NUMBER: 09/273,623
PRIOR FILING DATE: 1999-03-22
PRIOR FILING DATE: 1999-03-22
PRIOR FILING DATE: 1999-03-22
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US-10-653-047-447
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APPLICANT: Randy M.
APPLICANT: Michael
                                                                                                                                     NUMBER OF SEQ ID NOS: 7860
SOFTWARE: FastSEQ for Windows Version
SEQ ID NO 447
LENGTH: 575
                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 447, Application US/10653047 Publication No. US20040229367A1
Query Match
Best Local Similarity
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                                                                                                                            TYPE: DNA
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Sakari Kauppinen
Ib Groth Clausen
3.0%;
57.6%;
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 Score
Pred.
106.2; DB 18;
No. 3.9e-08;
             Length 575;
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US-10-425-115-137269
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: La Rosa, Thomas J.
APPLICANT: Kovalic, David K.
APPLICANT: Zhou, Yihua
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules a
TITLE OF INVENTION: Plants
FILE REFERENCE: 38-21(5322)B
FULE REFERENCE: 38-21(5322)B
CURRENT APPLICATION NUMBER: US/10/425,115
CURRENT FILING DATE: 2003-04-28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NUMBER OF SEQ ID NOS: 369326
SEQ ID NO 137269
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                                                                                                                                                                                                                                                                                  Matches 158;
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Best Local
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OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                LENGTH: 286
TYPE: DNA
ORGANISM: Zea mays
                                                                                                                                                                                                                                2055 TGAGAGATTATGTCGATGTTAGTGCTGATTGGTTATGTCTTATGCCTTAATCGATGAAATTA 2114
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                                                                                  CCGTTTTCACTGCTAGAGATACTGATTTTAGTAGTATGTTACAAAGAATTGGTGAATCAA 2234
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        GAAGAAAAGTCATGACTTTAATGAGATTATTATCAGGTAAAGCTGATGTCATTAAAATGT 2294
                                              ATGTGTTTGTTGCTCGCGTGGAAGATTTTGGTACTTTCTTGCCACGCATTGGCGACCTTC
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Pred. No. 8.8e-07;
0; Mismatches 101;
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US-10-363-345A-26081/c
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TITLE OF INVENTION: Method for determining the degree of methylation of defined
TITLE OF INVENTION: Cytosines in genomic DNA in the sequence context of 5'-CpG-3
FILE REFERENCE: E01/1227
CURRENT PELLICATION NUMBER: US/10/363,345A
CURRENT FILING DATE: 2003-03-03
NUMBER OF SEQ ID NOS: 40712
SEQ ID NO 26081
LENGTH: 969
TYPE: DNA
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 26081, Application US/10363345A
Publication No. US20040234960A1
GENERAL INFORMATION:
APPLICANT: Alexander Olek
APPLICANT: Christian Piepenbrock
APPLICANT: Kurt Berlin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 2.7%;
Best Local Similarity 48.2%;
Matches 355; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FEATURE:
OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)
OTHER INFORMATION: CpG-island No: 26081
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                                         CCAACCCCAATTATTACTAATGCTAATAAATCAAGAAGAAAATCTCAATTGGAAAATTTA 850
                                                                                                                      ACTGACGACAATTCTACTAATAATCATACTCATCTTGCAATTCCAATTCCAATTCCAATT 790
                                                                                                                                                                                                                                                                                                                                                                                             ANACCATTGACTCGTAAATCTGGTTCTTCAATTAAGAAAAATCTAATCTTACCGATAAA 613
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AAAACGAACGAAAATAAAAATAAAAATACTAATAAAACGAATAAAAATACGAATAAAAAT 321
                                                                                                                                                                           AATAAAAATATTAACGAAACGAATAAAAATACGAATAAAAATACTAATAAAAACGAATAAA 441
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                                                                                                                                                                                                                                                                  AATACTAATAAAACGAATAAAAATAAAATAAAAATAAAAATACTAATAAAAACGAATAAA 501
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## ALIGNMENTS

REFERENCE AUTHORS TITLE JOURNAL PUBMED REFERENCE AUTHORS REFERENCE AUTHORS ACCESSION VERSION KEYWORDS RESULT 1 CNS06173/c LOCUS DEFINITION SOURCE ORGANISM COMMENT JOURNAL MEDLINE PUBMED JOURNAL MEDLINE TITLE TITLE Submitted (07-SEP-2000) Genoscope - Centre National de Sequencage, 2 rue Gaston Cremieux, CP 5706, 91057 EVRY cedex, FRANCE. (E-mail: seqrefégenoscope.cns.fr - Web: www.genoscope.cns.fr) This GSS is part of a random genomic sequencing program of thirteen yeast species: Saccharomyces bayanus var. uvarum, Saccharomyces servazii, Zyosaccharomyces rouxii, saccharomyces servazii, Zyosaccharomyces rouxii, Saccharomyces Kluyveromyces thermotolerans, Kluyveromyces lactis var. lactis, Kluyveromyces marxianus var. marxianus, Pichia angusta, Debaryomyces hansenii var. hansenii, Pichia sorbitophila, Candida tropicalis and Yarrowia lipolytica. Genomic inserts of 3 to 5 kb were prepared and both extremities were sequenced. See keywords for description of this sequence and for the sequence of Bolotin-Fukuhara, M., Bon, E., Brottier, F., Casaregola, S., de Montigny, J., Dujon, B., Durrens, P., Lepingle, A., Llorente, B., Malpertuy, A., Neuveglise, C., Ozier-Kalogeropoulos, O., Potier, S., Saurin, W., Tekaia, F., Toffano-Nioche, C., Wesolowski-Louvel, M., Wincker, P. and Weissenbach, J. Genomic exploration of the hemiascomycetous yeasts: 1. A set of yeast species for molecular evolution studies

PEBS Lett. 487 (1), 3-12 (2000) 912 bp DNA linear GSS 30-NOV-201 T7 end of clone ASOAA018C10 of library ASOAA from strain CLIB 533 of Saccharomyces bayanus, genomic survey secuence AL399975 Aigle, M. and Durrens, P.
Genomic exploration of the hemiascomycetous yeasts: 5.
Saccharomyces bayanus var. uvarum
FEBS Lett. 487 (1), 37-41 (2000) Saccharomyces bayanus Saccharomyces bayanus 3 (bases 1 to 912) Genoscope. 20584715 2 (bases 1 to 912)
Bon, E., Neuveglise, C., 1 (bases 1 to 912)
Souciet, J.L., Aigle, M., Artiguenave, F., Blandin, G., Saccharomycetales; Saccharomycetaceae; Saccharomyces. Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes; AL399925 Direct Submission AL399925.1 GI:12155087 1152876 Casaregola, S., Artiguenave, F., Wincker, P., GSS 30-NOV-2001

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Location/Qualifiers
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/note="similar to Saccharomyces cerevisiae ORF YOL130w [
ALR1 , divalent cation transporter ]
1 putative frameshift(s)"
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complement(<2...>906)
/note="similar to Saccharomyces cerevisiae ORF YFL050c [
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/strain="CLIB 533"
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'clone="ASOAA018C10"
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68.9%;
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Bolotin-Fukuhara, M., Bon, B., Brottier, P., Casaregola, S.,
de-Montigny, J., Dujon, B., Durrens, P., Lepingle, A., Llorente, B.,
Malpertuy, A., Neuveglise, C., Ozier-Kalogeropoulos, O., Potier, S.,
Saurin, W., Tekaia, P., Toffano-Nioche, C., Wesolowski-Louvel, M.,
Wincker, P. and Weissenbach, J.
Genomic exploration of the hemiascomycetous yeasts: 1. A set of
yeast species for molecular evolution studies
PEBS Lett. 487 (1), 3-12 (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CNS0736W 1032 bp DNA linear GSS clone BA0AB017C04 of library BA0AB from strain CLIB 210 Kluyveromyces lactis, genomic survey sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            lactis var. lactis, Kluyveromyces marxianus var. marxianus, Pichia angusta, Debaryomyces hansenii var. hansenii, Pichia sorbitophila, Candida tropicalis and Yarrowia lipolytica. Genomic inserts of 3 to 5 kb were prepared and both extremities were sequenced. See keywords for description of this sequence and for the sequence of the other extremity of this insert.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Submitted (08-SEP-2000) Genoscope - Centre National de Sequencage, 2 rue Gaston Cremieux, CP 5706, 91057 EVRY cedex, FRANCE. (E-mail: segret@genoscope.cns.fr - Web: www.genoscope.cns.fr)
This GSS is part of a random genomic sequencing program of thirteen yeast species: Saccharomyces bayanus var. uvarum, Saccharomyces exiguus, Saccharomyces servazzii, Zygosaccharomyces rouxii, saccharomyces kluyveri, Kluyveromyces thermotolerans, Kluyveromyces
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bolotin-Fukuhara,M., Toffano-Nioche,C., Artiguenave,F., Duchateau-Nguyen,G., Lemaire,M., Marmeisse,R., Montrocher,R., Robert,C., Termier,M., Wincker,P. and Wesolowski-Louvel,M. Genomic exploration of the hemiascomycetous yeasts: 11.
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                                                                                                       similar to Saccharomyces cerevisiae ORF
divalent cation transporter ] "
/evidence=not_experimental
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                                                                                                                                                                                                                    complement(<3...>987)
/note="similar to Saccharomyces cerevisiae ORF YFL050c [
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/clone="BA0AB017C04"
/clone_lib="BA0AB"
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/strain="CLIB 210"
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Score 301.6; DB 9;
Pred. No. 1.1e-44;
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                                                 Casaregola, S., Neuveglise, C., Lepingle, A., Bon, E., I Artiguenave, F., Wincker, P. and Gaillardin, C. Genomic exploration of the hemiascomycetous yeasts:
                                                                                                                                    Genomic exploration of the hemiascomycetous yeasts: yeast species for molecular evolution studies FEBS Lett. 487 (1), 3-12 (2000)
                                                                                                                                                                           Bolotin-Fukuhara,M., Bon,B., Brottier,P., Casaregola,S., de-Montigny,J., Dujon,B., Durrens,P., Lepingle,A., Llorente,B., Malpertuy,A., Neuveglise,C., Ozier-Kalogeropoulos,O., Potier,S., Saurin,W., Tekala,F., Toffano-Nioche,C., Wesolowski-Louvel,M., Wincker,P. and Weissenbach,J.
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Yarrowia lipolytica
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336; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Submitted (07-SEP-2000) Genoscope - Centre National de Sequencage, 2 rue Gaston Cremieux, CP 5706, 91057 EVRY cedex, FRANCE. (E-mail: sequefogenoscope.cns.fr - Web: www.genoscope.cns.fr)
This GSS is part of a random genomic sequencing program of thirteen yeast species: Saccharomyces bayanus var. uvarum, Saccharomyces
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           exiguus, Saccharomyces servazzii, Zygosaccharomyces rouxii, Saccharomyces kluyveri, Kluyveromyces thermotolerans, Kluyveromyces lactis var. lactis, Kluyveromyces marxianus var. marxianus, Pichia angusta, Debaryomyces hansenii var. hansenii, Pichia sorbitophila,
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CTCTGACTATGATGCGTCTTCTATCCGGTAAGGCTGATGTTCGAATGTTTTGCCAAGC
                                                  TCATGACTTTAATGAGATTATTATCAGGTAAAGCTGATGTCATTAAAATGTTTGCTAAAA 2303
                                                                                                                                                                CTGCTAGAGATACTGATTTTAGTAGTATGTTACAAAGAATTGGTGAATCAAGAAGAAAAAG 2243
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nilarity 61.8%;
Conservative
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/clone="AWDAA006E08"
/clone_lib="AWDAA"
/note="end: T3"
/3: .>833
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/strain="CLIB 89"
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Pred. No. 3.3e-28;
0; Mismatches 208;
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RESULT 4
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Direct Submission

Submitted (08-SEP-2000) Genoscope - Centre National de Sequencage,
2 rue Gaston Cremieux, CP 5706, 91057 BVRY cedex, PRANCE. (E-mail:
seqref@genoscope.cns.fr - Web: www.genoscope.cns.fr)

This GSS is part of a random genomic sequencing program of thirteen
yeast species: Saccharomyces beyanus var. uvarum, Saccharomyces
exiguus, Saccharomyces servazzii, Zygosaccharomyces rouxii,
Saccharomyces kluyveri, Kluyveromyces thermotolerans, Kluyveromyces
lactis var. lactis, Kluyveromyces marxianus var. marxianus, Pichia
angusta, Debaryomyces hansenii var. hansenii, Pichia sorbitophila,
Candida tropicalis and Yarrowia lipolytica. Genomic inserts of 3 to
5 kb were prepared and both extremities were sequenced. See
keywords for description of this sequence and for the sequence of
the other extremity of this insert.
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Genomic exploration of the hemiascomycetous yeasts: 1. A set of yeast species for molecular evolution studies
FEBS Lett. 487 (1), 3-12 (2000)
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Bolotin-Fukuhara, M., Toffano-Nioche, C., Artiguenave, F.,
Duchateau. Nguyen, G., Lemaire, M., Marmeisse, R., Montrocher, R.,
Robert, C., Termier, M., Wincker, P. and Wesolowski-Louvel, M.
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2 (bases
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Kluyveromyces lactis
Kluyveromyces lactis
Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; Saccharomycetaceae; Kluyveromyces.

1 (bases 1 to 798)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Genomic exploration of the hemiascomycetous yeasts: 11. Kluyveromyces lactis
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                                                                                                                                   /db_xref="taxon:28985"
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/clone="BA0AB011C01"
/clone="BA0AB011C01"
/clone="Ba0AB011C01"
complement(<62...>796)
/note="similar to Saccharomyces cerevisiae ORF YFL050c
ALR2; divalent cation transprter |
similar to Saccharomyces cerevisiae ORF YOL130w [ ALR1 divalent cation transporter ] "
                                                                                                                                                                                                                                                                                                                                                                                                    /mol_type="genomic DNA"
/strain="CLIB 210"
                                                                                                           evidence=not_experimental
                                                                                                                                                                                                                                                                                                                                                                            variety="lactis"
                                                                                                                                                                                                                                                                                                                                                                                                                                                             organism="Kluyveromyces lactis"
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Score 210.8; DB 9;
Pred. No. 3.9e-28;
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1643 CCTGATAGATTTTCACTTTTCCATTCTGAATCAGAAGAAACTATTCATGCCCCCGATATT 1702

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Matches 253
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Bukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; mitosporic Saccharomycetales; Candida.
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                                                                                                                                                                                                                                                                                               Contact: Wong S
Department of Genetics,
Trinity College Dublin
Dublin 2, Ireland
                                                                                                                                                                                                                                                                                                                                                                                                                  Wong,S., Fares,M.A., Zimmermann,W., Butler,G. and Wolfe,K.H. Evidence from comparative genomics for a complete sexual cycle in the 'asexual' pathogenic yeast Candida glabrata
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                                                                                                                                                                                                                               Class: plasmid ends.
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                     Similarity
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/clone="CG1236"
/clone_lib="Candida glabrata Random Genomic Library"
                                                                                                                                                            organism="Candida glabrata"
/mol type="genomic DNA"
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Submitted (07-SEP-2000) Genoscope - Centre National de Sequencage, 2 rue Gaston Cremieux, CP 5706, 91057 EVRY cedex, FRANCE. (E-mail: seqref@genoscope.cns.fr - Web: www.genoscope.cns.fr) This GSS is part of a random genomic sequencing program of thirteen yeast species: Saccharomyces bayanus var. uvarum, Saccharomyces exiguus, Saccharomyces servazzii, Zygosaccharomyces rouxii, Saccharomyces kluyveri, Kluyveromyces thermotolerans, Kluyveromyces lactis var. lactis, Kluyveromyces marxianus var. marxianus, Pichia angusta, Debaryomyces hansenii var. hansenii, Pichia sorbitophila, Candida tropicalis and Yarrowia lipolytica. Genomic inserts of 3 to 5 kb were prepared and both extremities were sequenced. See keywords for description of this sequence and for the sequence of the other extremity of this insert.
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                                                                                                                                                                                                                                                         Direct Submission
Submitted (07-SEP-2000)
2 rue Gaston Cremieux. (
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AL399045.1 GI:12153045
GSS.
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ALR1; divalent cation transporter]"
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/clone="ASOAA012F12"
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Pred. No. 7.8e-24;
1; Mismatches 371;
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                                                                                Matches 255;
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                                                                                                           Local Similarity
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Submitted (07-SEP-2000) Genoscope - Centre National de Sequencage,
Submitted (07-SEP-2000) Genoscope - Centre National de Sequencage,
2 rue Gaston Cremieux, CP 5706, 91057 EVRY cedex, PRANCE. (E-mail:
8 eqref@genoscope.cns.fr - Web: www.genoscope.cns.fr)
This GSS is part of a random genomic sequencing program of thirteen
yeast species: Saccharomyces bayanus var. uvarum, Saccharomyces
exiguus, Saccharomyces servazzii, Zygosaccharomyces rouxii,
Saccharomyces kluyveri, Kluyveromyces thermotolerans, Kluyveromyces
lactis var. lactis, Kluyveromyces marxianus var. marxianus, Pichia
angusta, Debaryomyces hansenii var. hansenii, Pichia sorbitophila,
Candida tropicalis and Yarrowia lipolytica. Genomic inserts of 3 to
5 kb were prepared and both extremities were sequenced. See
keywords for description of this sequence and for the sequence of
the other extremity of this insert.
2610 CACGTCCAAGAGCTGATATTGCATTATATTTTAGGTGATATTCAAGATCATATAATCACCA 2669
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T3 end of
of Saccha
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Bolotin-Fukuhara, M., Bon, E., Brottier, P., Casaregola, S.,
de-Montigny, J., Dujon, B., Durrens, P., Lepingle, A., Llorente, B.,
Malpertuy, A., Neuveglise, C., Ozier-Kalogeropoulos, O., Potier, S.,
Saurin, W., Tekaia, F., Toffano-Nioche, C., Wesolowski-Louvel, M.,
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                                                                                   Conservative
                                                                                                                                                                                                                                  /note="similar to Saccharomyces cerevisiae ORF YOL130w
ALR1 ; divalent cation transporter ]"
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/clone="ASOAA007H07"
/clone_lib="ASOAA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                 organism="Saccharomyces bayanus"
|mol_type="genomic DNA"
|strain="CLIB 533"
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                                                                                                      5.0%;
                                                                                <u>,</u>
                                                                                                         Score 176; DB 9;
Pred. No. 8.6e-22;
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                                                                                Mismatches 110;
                                                                                                                              Length 874;
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13 end of clone AS0AA005H07 of library AS0AA from strain of Saccharomyces bayanus, genomic survey sequence.
AL397913
               Submitted (07-SEP-2000) Genoscope - Centre National de Sequencage, 2 rue Gaston Cremieux, CP 5706, 91057 EVRY cedex, FRANCE. (E-mail: sequefagenoscope.cns.fr - Web: www.genoscope.cns.fr)
This GSS is part of a random genomic sequencing program of thirteen yeast species: Saccharomyces bayanus var. uvarum, Saccharomyces exiguus, Saccharomyces servazii, Zygosaccharomyces rouxii, saccharomyces servazii, Zygosaccharomyces rouxii, Saccharomyces in Kluyveromyces harmotolerans, Kluyveromyces lactis var. lactis, Kluyveromyces marxianus var. marxianus, Pichia angusta, Debaryomyces hansenii var. hansenii, Pichia sorbitophila, Candida tropicalis and Yarrowia lipolytica. Genomic inserts of 3 to
                                                                                                                                                                                                                                                                                                                                                                                    FEBS Lett.
20584715
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Souciet, J.L., Aigle, M., Artiguenave, F., Blandin, G., Bolotin-Fukuhara, M., Bon, B., Brottier, P., Casaregola, S., de-Montigny, J., Dujon, B., Durrens, P., Lepingle, A., Llorente, B., Malpertuy, A., Neuveglise, C., Ozier-Kalogeropoulos, O., Potier, S. Saurin, W., Tekaia, F., Toffano-Nioche, C., Wesolowski-Louvel, M.,
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PEBS Lett. 487 (1), 3-12 (2000)
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  and both extremities were sequenced.
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                              Coccidioides posadasii
Coccidioides posadasii
Coccidioides posadasii
Eukaryota; Pungi, Ascomycota; Pezizomycotina; Eurotiomycetes;
Eukaryota; Pungi, Ascomycota; Coccidioides.

Onygenales; mitosporic Onygenales; Coccidioides.

1 (bases 1 to 955)
Gardner,M.J. and Cole,G.T.
Analysis of gene expression in Coccidioides posadasii mycelia apherules via expressed sequence tags
Unpublished (2003)
Other_ESTs: EST807319
                                                                                                                                                                                                                                                          CO028936 955 bp mRNA linear EST 10-JUN-2004 EST807320 Coccidioides posadasii spherule cDNA library, 0.5 to 5.3 kb Coccidioides posadasii cDNA clone CIFAU87 5' end, mRNA sequence.
Contact: Gardner MJ
The Institute for Genomic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     keywords for description of this sequence and for the other extremity of this insert.
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/mol_type="genomic DNA"
/strain="CLIB 533"
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Pred. No. 8.6e-22;
0; Mismatches 110;
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EST837214 Aspergillus flavus Normalized cDNA
Aspergillus flavus cDNA clone NAFEQ83 5' end
Aspergillus flavus
Aspergillus flavus
Aspergillus flavus
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
Eukaryota; Trichocomaceae; mitosporic Trichocomaceae; Asperg
1 (bases 1 to 387)
Yu,J., Whitelaw,C.A., Nierman,W.C., Bhatnagar,D. and Clevelan
                                                                                                           Aspergillus Élavus cDNA clone NAFEQ8
Hypothetical protein, mRNA sequence.
CO142543.
CO142543.1 GI:48896544
                                                                                              EST.
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Coccidioides posadasii spherule cDNA library, 0.5
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0.5 to 5.3 kb"
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/lab_host="E. coli DH10B,
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Pred. No. 3.9e-21;
0; Mismatches 156;
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BACKWARD: M13R
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USDA/ARS, Southern Regional Research Center
1100 Robert E. Lee Boulevard, New Orleans, 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Aspergillus flavus expressed sequence tags for identification genes with putative roles in aflatoxin contamination of crops FEMS Microbiol. Lett. (2004) In press
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Email: jiuyu@srrc.ars.usda.gov
Contact Dr. Yu at USDA/ARS SRRC (jiuyu@srrc.ars.usda.gov) for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Tel: 504 286 4405
Fax: 504 286 4419
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GTACTTGTCCTACTGATTCGGAAATGAAAATGTTGGCCAAAGCATTTGGTATTCATCCTT 1835
                               TCCAGTCTATTGAGGATGA
                                                                                                                                                                         CACCTCACCCGGCGAATGTGCGCCGGCGAATCCGTCAACTAATGGACTACTTAATCCTCA
                                                                                                                                                                                                            TTTCTCATCCAGCAAATGTTAGAAGAAGAGTTCGTCAATTGAGAGATTATGTCGATGTTA
                                                                                                                                                                                                                                                                                   CGATAAATGTTTATATTGTTTTTCCATGATGGTATATTAACGTTCCATTTTTCACCAA 2015
                                                                                                                                                                                                                                                                                                                    ATTATTTTGTCAATTATCGGACCTTCGACCAAGACCCAAATAGTGAGAACTATCTGCAAC
                                                                                                                                                                                                                                                                                                                                                     ATTATTTTGTTTGTTTCCATACTTTTGAAGCTGATAAAGAATCTGAAGATTATTTAGAAC
                                                                                                                                                                                                                                                                                                                                                                                          TCACGGCAGAGGATATCATGATGCAAGAGGCACGGGAAAAGTTGAACTGTTTCGGAATT
                                                                                                                                                                                                                                                                                                                                                                                                                                                             GTTCTTCTCCTACGGATGCAGAGATGCGAGTGATTGCCAAAGCCTTCGGGGTCCACGCGC
                                                                TTCATGGAATTGAATATGA
                                                                                                     GTTCTGATTGGATATCGTATGCCATAATTGATGATATTACTGATGTCTTCGGCCCGCTGA
                                                                                                                                      GTGCTGATTGGTTATGTTATGCCTTAATCGATGAAATTACCGATGGTTTTGCCCCCGTGA 2135
                                                                                                                                                                                                                                                CAGTGAATATGTACGTGGTTGTGTTCCGGGAAGGAGTCTTGTCCTTCCACTTTTCTCAGA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note="vector: pBlueScript (SK+) (Stratagene), antibiotic selection marker: Carbenicillin; Site 1: Not!, at the 5 prime end; Site 2: BCORI, at the 3 prime end; This normalized cDNA expression library was constructed using a mixture of mycelial cells grown under eight different medium conditions and harvested at 5 time points (18, 24, 48, 72, 96 hours). The poly-A sequence was trimmed off before ligating to vector."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           organism="Aspergillus
/mol_type="mRNA"
/strain="NRRL 3357"
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lab_host="E coli DH10B T1 resistant cells"
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clone="NAFEQ83"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 4.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      type="mycelia"
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                                                                  2154
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Pred. No. 2e-19;
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COMMENT
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CF709049
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Unpublished (2003)
Other_ESTs: CCAGA79TF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Cryptococcus neoformans var. neoformans
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Email: crypt@tigr.org
Seq primer: TR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Tel: 301-838-3543
Fax: 301-838-0208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Department of Eukaryotic Rockville, MD 20850, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Contact: Brendan Loftus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Fungi; Basidiomycota; Hymenomycetes;
Heterobasidiomycetes; Tremellomycetidae; Tremel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Cryptococcus neoformans
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CF709049.1 GI:41563208
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                                                                                                                                                                                                                                                                                                                                                         CATTIGGTATICATICATITAACIGCIGAAGATATICGAAIGCAAGAAACICGIGAAAAAG 1877
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                                                                                                                                                                         CGTTCCATTTTTCACCAATTTCTCATCCAGCAAATGTTAGAAGAAGAGTTCGTCAATTGA 2057
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                                   ATGGTTTTGCCCCCGTG 2134
                                                                  AAGACTACATTTCCGTGACTTCTGACTGGATCTCTTACGCCCTTATCGATGACATCACCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   sequencing of clones
21 cDNA library
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /clone_lib="C.neoformans strain JEC21"
/note="Vector: pCMVSport6; Site_1: Not1 EcoRV; The full
length, normalized library was prepared from a variety of
conditions using RNA provided by Joseph Heitman and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Jennifer Lodge"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /db_xref="taxon:40410"
/clone="CCAGA79"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  strain="JEC21"
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 771
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Pred. No. 3.5e-18;
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                                                                                                                                                                                                                                                                                                  misc_feature
                                                                                                     Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Submitted (07-SEP-2000) Genoscope - Centre National de Sequencage,
2 rue Gaston Cremieux, C 5-706, 91057 ENVRY cedex, FRANCE. (E-mail:
8 seqref@genoscope.cns.fr - Web: www.genoscope.cns.fr)
This GSS is part of a random genomic sequencing program of thirteen
yeast species: Saccharomyces bayanus var. uvarum, Saccharomyces
exiguus, Saccharomyces servazzii, Zygosaccharomyces rouxii,
Saccharomyces kluyveri, Kluyveromyces thermotolerans, Kluyveromyces
lactis var. lactis, Kluyveromyces marxianus var. marxianus, Pichia
angusta, Debaryomyces hansenii var. hansenii, Pichia sorbitophila,
Candida tropicalis and Yarrowia lipolytica. Genomic inserts of 3 to
5 kb were prepared and both extremities were sequenced. See
keywords for description of this sequence and for the sequence of
the other extremity of this insert.
1616 TCTGATGGGATTAATGGAGGTTCATTACCTGATAGATTTTCACTTTTTCCATTCTGAATCA 1675
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Bon,E., Neuveglise,C., Casaregola,S., Artiguenave,r. Aigle,M. and Durrens,P.
Genomic exploration of the hemiascomycetous yeasts:
Saccharomyces bayanus var. uvarum
FEBS Lett. 487 (1), 37-41 (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CNS06GSK
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Bolotin-Fukuhara, M., Bon, E., Brottier, P., Casaregola, S.,
de-Montigny, J., Dujon, B., Durrens, P., Lepingle, A., Llorente, B.,
Malpertuy, A., Neuveglise, C., Ozier-Kalogeropoulos, O., Potier, S.
Saurin, W., Tekaia, F., Toffano-Nioche, C., Wesolowski-Louvel, M.,
Wincker, P. and Weissenbach, J.
Genomic exploration of the hemiascomycetous yeasts: 1. A set of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Saccharomyces bayanus
Saccharomyces bayanus
Saccharomyces bayanus
Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; Saccharomycetaceae; Saccharomyces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AL398106
AL398106.1 GI:12151311
GSS.
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end of clone AS0AA007A08 of library AS0AA from strain CLIB 533
Saccharomyces bayanus, genomic survey sequence.
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                                                                                 Conservative
                                                                                                                                                                                                    l putative frameshift(s)"
/evidence=not_experimental
                                                                                                                                                                                                                                                        ALR1 ; divalent cation transporter ]
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                                                                                                                                                                                                                                                                                                                                                         /db_xref="taxon:4931"
/clone="ASOAA007A08"
/clone_lib="ASOAA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                            /mol_type="genomic
/strain="CLIB 533"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        organism="Saccharomyces bayanus
                                                                                                                                                                                                                                                                               note="similar to Saccharomyces cerevisiae ORF YOL130w [
                                                                                                                                                                                                                                                                                                                                                                                                                                    'variety="uvarum"
                                                                                                                                                                                                                                                                                                            . >953
                                                                                                   4.1%;
                                                                           Score 146; DB 9;
Pred. No. 2.6e-16;
2; Mismatches 87
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                                                                                 87;
                                                                                                                          Length 973;
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Best Local
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                                                                                                                                        2667 CCATGTTTCAAAATTTATTAGCCTATGAAAAAAATTTTCAGTCGTTCACATTCAAATTATT
   2787 AAATTACTTTGATTGGGACAATGTTAGTTCCATTAAATTTAGTCACGGGACTTTTTGGTA 2846
                                                                       2727 TAGCTCAATTACAAGTTGAATCATTCAATTCCAATAATAAAATCACCGAAATGTTTTCTA 2786
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BZ297820
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Wong,S., Fares,M.A., Zimmermann,W., Butler,G. and Wolfe,K.H. Evidence from comparative genomics for a complete sexual cycle the 'asexual' pathogenic yeast Candida glabrata Genome Biol. 4 (2), R10 (2003)
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Candida glabrata
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Dublin<sup>2</sup>, Ireland
Tel: 353 1 6082319
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Trinity College Dublin
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Department of Genetics,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Fungi; Ascomycota;
Saccharomycetales; mitosporic
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                                                                                                                                                                                 ATACACAACCAAGAGGTGATATCGCGCTGTATCTAGGTGACATCCAGGATCATTTACTGA
                                                                                                                                                                                                          ATGCACGTCCAAGAGCTGATATTGCATTATATTTAGGTGATATTCAAGATCATAATCA
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                                       TAGCACAACTTCAAGTGGAATCCTTCAACTCCAACAACAAAGTCACAGAAATGCTTGGTA
                                                                                                             CAATGTATCAAAACTTATCAGCTTATGAAAAGATTTTTTCTAGATCACATACCANGTACT
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                                                                                                                                                                                                                                                         Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                 /organism="Candida
/mol_type="genomic
/strain="CBS 138"
                                                                                                                                                                                                                                                                                                                                           /db_xref="taxon:5478"
/clone="CG3653"
/clone_lib="Candida glabrata Random Genomic
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Pred. No. 3.3e-16;
D; Mismatches 62
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Best Local Similarity
Matches 311; Conserv
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Insert Length: 800 Std Error:
Seq primer: M13 reverse.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Rothamsted Research,
Harpenden, Herts, UNITED KINGDOM
Tel: +44(0)1582 763133
Fax: +44(0)1582 760981
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 (bases 1 to 763)
Keon, J.P.R., Hargreaves, J.A., Antoniw, J.F. and Hammond-Kosack, K.
Analysis of expressed sequence tags from the wheat fungal leaf
blotch pathogen, Mycosphaerella graminicola (anamorph Septoria
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AJ637812 MgC Mycosphaerella graminicola cDNA clone mgc01d10f, mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Fungal Genet. Biol. (2004) In press Contact: Keon J
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Bukaryota; Fungi; Ascomycota; Pezizomycotina; Dothideomycetes
Chaetothyriomycetes incertae sedis; Mycosphaerellaceae;
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Mycosphaerella graminicola
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                                                                                         GAAGATTATTTAGAACCGATAAATGTTTATATTGTTGTTTTCCATGATGGTATATTAACG
                                                                                                                                  CTGTTCAAGAGCTACTACTTCCTGCTTCCGCAGCTTCTATGCGGTGGACAAGGAAAGC
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                                                                                                                                                                                                     CGCGTCCATCCTTTGACTCGAGAGGATATCACCACGCAGGAGACACGTGAAAAAGTCGAG
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                             TTCCATTTTTCACCAATTTCTCATCCAGCAAATGTTAGAAGAAGTTCGTCAATTGAGA 2059
                                                                 GAGGACTACCTGGAGCCAATTAACATTTACGCCGTCGTCTTCCGCGAAGGTCTGCTCACG
                                                                                                                                                                                                                                                                      TGGTGGCTGGACATGCTCAACCCGTCGGAGGAGGAGATCTTTGCCATCTGCAGCGCCTTC
TTCTCCTTCTGCCAGAACCACCACGCCGCCACAGTCCGCAAGCGTATCGGTCGTCTTCGC
                                                                                                                                                                                                                                                                                                                                       Conservative
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/strain="Strit"
/db_xref=""
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/clone="mgc0ld10f"
/clone="lb="MgC"
/clone="Yector: pSPORT1; Library constructed from senescent /note="Vector: pSPORT1; Library constructed from senescent wheat leaves 21-25 days after infection with Mycosphaerella graminicola_exhibiting abundant hyphal
                                                                                                                                                                                                                                                                                                                                                                                                                         growth and asexual sporulation"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /organism="Mycosphaerella graminicola"
/mol_type="mRNA"
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                                                                                                                                                                                                                                                                                                                                                       Score 143;
Pred. No.
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4.0%;
Best Local Similarity 59.0%;
Matches 242; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Tel: + 33 383 39 40 13
Fax: + 33 383 39 40 69
Email: duplessi@nancy.inra.fr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 (bases 1 to 614)
Lacourt, I., Duplessis, S., Abba, S., Bonfante, P. and Martin, F. Isolation and characterization of differentially expressed gmycelium and fruit body of Tuber borchil
Unpublished (2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Tuber borchi
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Contact: Duplessis S
UMR 1136 INRA/UHP Interactions Arbres/Micro-Organismes
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Pezizales; Tuberaceae; Tuber.
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                                                                                                                               /dev stage="vegstative hyphae" / clone lib="conA library of Tuber borchii vegetative / clone lib="conA library of Tuber borchii vegetative mycelium grown on MMN liquid medium" / note="Organ: mycelium; Vector: pBK-CMV phagemid; Site 1: RooRI; Site 2: Xhol; The cDNA library was constructed from total RNA of Tuber borchii mycelium grown on MMN liquid medium using the UnizapxR cDNA library System Construction kit (Stratagene, USA) according to the manufacturer's instructions. UnizapXR clones were converted to pBK-CMV phagemid clones using E. coli BM25.8 as the bacterial host"
                                                                                                                                                                                                                                                                                                                                                                                                                                       /organism="Tuber borchii"
/mol_type="mRNA"
/db_xref="taxon:42251"
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498	CTTTTCCGGTCATACTATTTTGTATGCTTCCGCTCTTTTGTGCAAAATAAGAATTCGCCA	439	ğ
1942	TTATTTAAAAGTTATTTATTTTGTTTTGCATACTTTTGAAGCTGATAAAGAATCTGAA	1883	₹
438	GCAATCCACCCCTTGACCGCCGAGGATATTCGGGTTCAGGAGACCCGCGAGAAAGTTGAA	379	ğ
1882	GGTATTCATCCTTTAACTGCTGAAGATATTCGAATGCAAGAAACTCGTGAAAAAGTTGAA	1823	¥
78	TGGTGGTTGGATTGTTACAATCCTACTACTGAAGAATTGGCTATGCTCATGAAGGCTTTT 378	319	Ծ
1822	TGGTGGTTAGATTGTACTTGTCCTACTGATTCGGAAATGAAAATGTTGGCCAAAGCATTT	1763	₹
318	GGCGACCTCCTATGCGATGGTGAGAATTTCCACGACCTCTTCCCGGGGTGGGCAAGGTGTC	259	ğ
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Search completed: April 14, 2005, 22:05:42 Job time: 10852 secs

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BD273775 Identification of candida albicans and use thereof in antifungal drug BD273775 BD273775.1 GI:33083543 JP 2002543799-A/2. Candida albicans Candida albicans Eukaryota; Fungi; Ascomycota; Sacc Saccharomycetales; mitosporic Sacc		6 170800 2		.6 28600 8	.6 3957 8	.6 203127 5	.7 115990 5	145553 5	.0 145306 2	.0 143342 2	.0 177575 5	.1 155204 2	.1 34347 2		2 94534 5	.3 110000 8	8 537	537 6	8 537 6	8 110000 8	211113 2	9 163843 5 B	11	.4 110000 8	
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REFERENCE AUTHORS TITLE FEATURES source COMMENT Query Match 99.9%; Score 3523; I Best Local Similarity 100.0%; Pred. No. 0; Matches 3525; Conservative 0; Mismatches JOURNAL Saccharomycetales; mitosporic Saccharomycetales
1 (bases 1 to 3525)
Roemer, T., Bussey, H. and Davison, J.
Identification of candida albicans essential furol and use thereof in antifungal drug discovery Patent: JP 2002543799-A 2 24-DEC-2002;
MCGILL UNIVERSITY
OS Candida albicans
PN JP 2002543799-A)2
PD 24-DEC-2002
PF 05-MAY-2000 JP 2000616385
PR 05-MAY-1999 US 60/132878
PI TERRY ROEMER, HOWARD BUSSEY, JOHN DAVISON PC C12N15/09, COTK14/40, C07K16/14, C12Q1/68, G011 G01N3J/569,
PC C12N15/09, COTK14/40, C07K16/14, C12Q1/68, G011 G01N3J/569, genes and use
thereof in antifungal drug discovery
Key
Location/Qualifiers
CDS (338) /2222 Candida albicans
JP 2002543799-A/2
24-D8C-2502
25-D8C-2002
05-MAY-2000 JP 2000616385
05-MAY-1999 US 60/132878
TERRY ROEMER, HOWARD BUSSEY, JOHN DAVISON
C12N15/09, C07K14/40, C07K16/14, C12Q1/68, G01N33/15, G01N33/50, Identification of candida albicans essential fungal specific Location/Qualifiers
1. .3525 /organism="Candida albicans" /mol\_type="genomic DNA" /db\_xref="taxon:5476" DB 6 Length 3525; fungal specific genes g

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901 TGAAAATGATTTAGTTAGTCCCATGACAAAATGAAAACTAATGATAGTGAAAATTAC 960	721 AAAAGATAATACTGACGACAATTCTACTAATAATCATCATCTTGCAATTCCAATTCC 780	541 ATCAGATAANGCTAAACCATTGACTCGTAGATTCTGTTCTTCAATTAGAAAAAATCTAA 600	361 TCAAAATTCAACTAATCAACCTATTCCTACATCATGAAGTATTGAATAGTAACTAATTCAACTAATCAACTATCCTACTATTCCTAGATGATAGTATATTGAACTAATTCAACTAATCAACCTATTCCTAGATCTAATCTAATCAACTAATCAACCTATTCCTAGATCTGATGAAGTATTGGATGATCATAG 420 361 TCAAAATTCAACTAATCAACCTATTCCTAGATCTGATGAAGTATTGGATGATTAGATCATAG 420 421 AAATCAAATCACTAATGATTGTGCCATTAGTGATAGTGAAGATGAGTTGGAATTAAAATC 480 421 AAATCAAATCACTAATGATTGTGCCATTAGTGAATAGATGAGTTGGAATTAAAATC 480 481 AGAATTAGAATCAGAAGTTGTAAAAAGCGAAAAAACAACAACAACATCATCAAGAGATTAC 540 481 AGAATTAGAATCAGAAGTTGTAAAAAGCGAAAAAACAACAACAACAACAACAAGAGATTAC 540 481 AGAATTAGAATCAGAAGTTGTAAAAAAGCGAAAAAAACAACAACAACAACAACAAGAGATTAC 540	TWITCCATTITITITITACCCAAGCTATGAAAATTATTTTGTTGTCTAACAACTATA	1 TATATAATATATATATATATAAACATAACATATTAAAAAA
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  Query Match 99.9%; S
Best Local Similarity 100.0%;
Matches 3525; Conservative 0;
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Sequence 3 from Patent W00068420.
AX046919
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Identification of candida albicans essential
and use thereof in antifungal drug discovery
Patent: WO 0068420-A 3 16-NOV-2000;
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Saccharomycetales; mitosporic Saccharomycetales; Candida.
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| translation="MSDESEY YONSTINOPIPRSDEVLDDHRNQITNDCAISDSEDEL
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| GGDDTINSGHKNRNYNMSSLRKDFYLKDNTDDNSTNNHTHLAIPIPIPIPIPIPII ITNAN
| KSRRKSOLENLPPLIKKKTIGHNISNNFENDLVSPMTKWKTINDSEDITNTSTTANHWK
| LGIGATTLGVGTGTTATATATAAAGRRPSRSSIDSEASSASSETEEDVCFPWVG
| DHIRVNGIDFDRIDEFIREERERAYLOKOMIAKNISTIDEFONLSKNNTTSGASRHPY
| HHHSNNNKKNNGGDDGGGSSMAALKYPPSNILIKKTLSRTEFTHBNSSSSERIFELKTKO
| QPPYKYDDQLSLTSSTSSTSGSGSQVKFGGARISDINGGSLPDRFSLFHSESEETI
| HAPDIPSLVSPGGSVRDLFRNGEETWHLDCTCPTDSEKKMALAKAPGIHPLFAEDLEMO
| ETREKVELFKSYYFVCFHTFEADKESEDYLEPINVYIVVFDGILTFHFSPISHPANV
| RRRVRQLEDYUDVSADMLCYALIDEITDGFAPVIHGIEYEADALEDAVFTARDTDFSS
| MLQRIGESRRKVMTLMRLLSGKADVIKMFAKRCQEEANSSSGYYQRQNNLQQQQAP
| PPPRNPITTSPINSTLLNUSLGTSTGGGVGVGGINFGRNFTGNNTNTNTNTTGSPSPP
| QQQQQHGITNKSPPIDARFRADIALYLGDIODHITTMFQNLLAVEKIFERSHSNYLA
| QLQVESFNSNNKITEMFSKITLIGTMLVPLNLVTGLFGMNVRVPGEGGTNLGWFFGIV
| GVLLFFISFFFAQWWLKKLNNSIEGQNNGNRPIFNHSSRRSRRSRRSIKAGKSI
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Location/Qualifiers
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mol_type="unassigned DNA"

/db_xref="taxon:5476"

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/transI_table=12
/protein_id="CAC18924.1"
/db_xxef="GI:11876350"
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2041 AAGAGTTCGTCAATTGAGAGATTATGTCGATGTTAGTGCTGATTGTTATGCCTT	Oy 1861 AGAAACTCGTGAAAAAGTTGATTATTATATTTTGTTTGCATACTTT 1920	Qy 1681 AACTATTCATGCCCCGATATTCCATCATTAGTATCACCAGGTCAATCTCTTCGAGATTT 1740		Db 1321 TĠCATCTCĠTCATCATCATCACCAGATAĀĀĀĀĀĀĀĀĀĀĀĀĀĀĀĀĀĀĀĀĀ	Qy 1141 AGATGTTTGTTTTCCTATGGTTGATCATATTAGAGTTAATGGAATTGATGA 1200

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Qy 633 TGAGTTTATCTGGTGGTGATGATACTATTAACAGCGGTCACAAAAATCGTAATTATAACA 692	Qy         465 ACTTGGAATTAAAATCAGAATTAGAATCAGAAGTTGTAAAAAGCGGAAA	345 ATAGTGAAAGTTATTATCAAAATTCAACTAATCAACCTATTCCTAGATCTGATGAAG 4	Query Match Query Match Best Local Similarity 97.2%; Pred. No. 4e-292; Best Local Similarity 97.2%; Pred. No. 4e-292; Matches 2293; Conservative 0; Mismatches 23; Indels 44; Gaps 8;  Qy 285 ATADATATATATATATCTCCCCTTTTGTTTTTTTTTCTCCCAGCCATGTCCG 344	ORGANISM Unknown. Unclassified.  REFERENCE 1 (bases 1 to 2358) AUTHORS Weinstock, K.G. and Bush, D. TITLE Nucleic acid sequences relating to Candida albicans for diagnostics and therapeutics and therapeutics and therapeutics Patent: US 6747137-A 6328 08-JUN-2004; FEATURES Location/Qualifiers Source /organism="unknown" /mol_type="genomic DNA"	RESULT 4 AR551197 AR551197 AR551197 DEFINITION Sequence 6328 from patent US 6747137. ACCESSION AR551197 VERSION AR551197 KEYMORDS KEYMORDS SOURCE Unknown.	Db 2641 ATTGAAGGACAAAATAATGGTAATCAACAATTTTTAATCAATC
Db 1439 CCCCGATATICCATCATTAGTATCACCAGGTCAATCTGTTCGAAAATGTAAAATGTTGA 1811  Qy 1752 GTGAAGAAACTTGGTGGTGGTTAGAATTGTACTTGTACTTAGTAAAATGTTAG 1811  Qy 1752 GTGAAGAAACTTGGTGGTTAGATTGTACTTGTACTTGTCCTACTGATTCGGAAATGAAAATGTTGG 1811  Db 1499 GTGAAGAAACTTGGTGTTAGATTGTACTTGTCCTACTGATTCGGAAATGAAAATGTTGG 1858  Qy 1812 CCAAAGCATTTGGTATTCATCCTTTAACTGCTGAAAAATGTAAAACTCGTG 1871  Db 1559 CCAAAGCATTTGGTATTCATCCTTTAACTGCCGAAGATATTCGAATGCAAGAAACTCGTG 1618  Qy 1872 AAAAAGTTGAATTATTTAAAAAGTTATTTTTTTTTTTCCATACTTTTGAAGCTGATA 1931		Qy 1398 TGGCAGCATTAAAATATACTCCAAAAAATATTTTAAAGAAAACATTATCAAGATTTGAAT 1457	Qy 1281 ATGAATTTCAAAATCTTTCCAAAAATAATACTACTAGTGGTGCATCCGTCATCCATATC 1340	Qy 1101 CTGATTCTCATGCATCAGAACTGAAGAACTGAAGAACATGTTTGTT	Oy 990 AACTTGGTATTGGTGCTACAACCCTTGGTGTTAGAACTGGTACTACCGCCACTGCCACTG	OY  813 CTAATAAATCAAGAAGAAAATCTCAATTGGAAAATTTAACTCCACTTAATTAA

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TTGGGGTTATGTGTGCTATAGTTATTGTTGCTGTAGTTTCTGCACGTATTTGGATCCTGA
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Weinstock, K.G. and Bush, D.
Nucleic acid sequences relating to Candida
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Patent: US 6747137-A 6327 08-JUN-2004;
Docation/Qualifiers
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TGAAAAAATTGAATAATTCAATTGAAGGACAAAATAATGGTAATCGACCAATTTTTAATC
                                                                                                   TITITGGTATGAATGTAAGAGTCCCTGGTGAAGGTGGTACCAATITTAGGTTGGTITTTCG
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                                                    GAATTGTTGGAGTATTAATATTTATAATTATTGGATCATTTATATTTGCTCAATGGTGGT
                                                                  GAATTGTTGGAGTATTAATATTTATTAATTATTGGATCATTTATATTTTGCTCAATGGTGGT
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/mol_type="genomic
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Cambridge, MA 02141, USA
Cambridge, MA 02141, USA
This clone is part of a collection of Saccharomyces cerevisiae
full-length ORF clones generated by the Harvard Institute of
full-length ORF clones generated by the Harvard Institute of
Proteomics Bach CDS has been cloned with its native stop-codon.
The CDS has been directionally cloned using the Gateway cloning
system into the donor vectors poons 201 or poons 221. Additional
system into the clone: 'TCCAGCTGACCACC' after the attl site as
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Marsischky,G., Rolfs,A., Richardson,A., Kane,M., Baqui,M., Taycher,E., Hu,Y., Vannberg,F., Weger,J., Kramer,J., Moreira,D., Kelley,F., Zuo,D., Raphael,J., Hogle,C., Jepson,D., Williamson,J., Camargo,A., Gonzaga,L., Vasconcelos,A.T., Simpson,A., Kolodner,R., Harlow,E. and Labaer,J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Marsischky,G., Rolfs,A., Richardson,A., Kane,M., Baqui,M.,
Taycher,E., Hu,Y., Vannberg,F., Weger,J., Kramer,J., Moreira,D.,
Kelley,F., Zuo,D., Raphael,J., Hogle,C., Jepson,D., Williamson,J.,
Kelley,F., Zoo,D., Raphael,J., Hogle,C., Jepson,D., Williamson,J.,
Camargo,A., Gonzaga,L., Vacconcelos,A.T., Simpson,A., Kolodner,R.,
Harlow,E. and Labaer,J.
Creation of the YFLEX clone resource: cloning of Saccharomyces
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Submitted (20-JUL-2004) Biological Chemistry and Molecular Pharmacology, Harvard Institute of Proteomics, 320 Charles st.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes; Saccharomycetales; Saccharomycetaceae; Saccharomyces.
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Yeast ORF Project.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 sequences in the clone: 'TCCAGCTGACCACC' after the attL1 site and before the 'ATG' (from Research Genetics primers used to amplify the ORFs, including a Kozak consensus sequence); 'ATCCCCGGGAATTGCCATG' after the stop codon and before the attL2 site (from the Research Genetics primers used to amplify the ORFs)
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/db_xref="GE-S1012975"
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ETVAHHQLRASAILITSNARPSRLAHSMHQRQLYVESNIHTPEDVVGYKRDYTMSSST
ASSGNKSKLSASSSASPITKVRKSELUSPVLEIPHESKSDTHSKLAKSKKATYSTTSA
ASSINPAYLLTKSTSQKSDADDDTLERKEVRMTRASFDSDVSQASROSQETEBDVCF
MPPQLHTRVNGIDFDSLEEYAQFANAEKSQFLASLQVPNBQKYSNVSQDIGFTSSTE
TSGSSAALKYTPRVSQTGEKSSESTNETEIHEKKEDEHEKKFSLHPGISFGKNKVEGE
TSGSSAALKYTPRVSQTGEKSSESTNETEIHEKKEDEHEKINSTHOTOSIVERGCTTFVFLFRG
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GEPTWWLDCSCPTDDEMRCIAKAFGIHPLTAEDIRMQETREKVELFKSYYFVCFHTFE
NDKESEDFLEPINVYIVVCRSGVLTFHFGPISHCANVRRRVRQLRDYVNVNSDWLCYA
LIDDITDSFAFVIQSIEYBADALEDSVFWARDWDFAAMLQRIGESRRKTMTLAFLLSG
KADVIKMFARKCODEANGIGFALTSQIRIALALQARQDNASHIKNUSSTTVPUNVAPTT
SQPRGDIALYLGDIQDHLLTMFQNLLAYEKIFSRSHTNYLAQLQVESFNSNNKVTEML
GKVTMIGTMLVFLNVITGLFGMNVKVPDENSSIAWWFGILGVLLLAVLGWFLASYWI
KRIDPPATLNEAAESGAKSVISSFLPKRNKRFNDRSKNINVRAGPSNKSVASLPSRYS
RYD"
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RYD"

942

/note="compared to SGD sequence"

/replace="g"

11.2%;

Score 396; Pred. No.

4e-46;

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8

Length 2580;

GATTTATTTAGAAATGGTGAAGAAACTTGGTGGTTAGATTGGTACTTGTCCTACTGATTCG 1795 GAAGAAACTATTCATGCCCCCGATATTCCATCATTAGTATCACCAGGTCAATCTGTTCGA 1735 ATGCAAGAAACTCGTGAAAAAGTTGAATTATTTAAAAGTTATTATTTTGTTTTGTTTCCAT 1915 GAAATGAAAATGTTGGCCAAAGCATTTGGTATTCATCCTTTAACTGCTGAAGATATTCGA 1855 GAATTATTCAGGGGAGGTGAGCCAACATGGTGGTTAGATTGTAGTTGTCCAACTGATGAT 1395 GATGAAACCGTTCATGCTAGTGATATCCCTTCCTTAGTGTCTGAGGGACAAACATTCTAT 1335 GCTGATGTCATTAAAATGTTTGCTAAAAGATGTCAAGAAGAAGAAGCTAAT 2323 CAAAGAATTGGTGAAAGTAGGCGTAAGACAATGACGTTGATGAGACTTCTTAGTGGTAAG 1875 CAAAGAATTGGTGAATCAAGAAAAGTCATGACTTTAATGAGATTATTATCAGGTAAA 2275 GCAGATGCAATCGAAGATTCTGTGTTCATGGCTCGTGACATGGATTTTGCAGCAATGTTA GCTGATGCCATTGAAGATGCCGTTTTCACTGCTAGAGATACTGATTTTAGTAGTATGTTA 2215 GCTTTAATCGATGACATTACTGATAGTTTCGCTCCTGTAATTCAATCTATTGAATATGAA GCCTTAATCGATGAAATTACCGATGGTTTTGCCCCCGTGATTCATGGAATTTGAATATGAA AGAAGAAGAGTTCGTCAATTGAGAGATTATGTCGATGTTAGTGCTGATTGGTTATGTTAT 2095 GTCTGTAGGTCAGGTGTTTTAACATTCCATTTTGGCCCCAATATCTCATTGTGCTAATGTC 1635 GTTTTCCATGATGGTATATTAACGTTCCATTTTTCACCAATTTCTCATCCAGCAAATGTT 2035 **ACCTTTGAAAATGATAAAGAATCAGAGGATTTTCCTGGAACCTATTAACGTTTACATTGTT** ACTTTTGAAGCTGATAAAGAATCTGAAGATTATTTAGAACCGATAAATGTTTATATATTGTT TCTTACCAGGGTACAGACTTTCAAATTCCTAATAGATTTTCTTTTTTTCTGTTCCGAATCT TCTGATGGGATTAATGGAGGTTCATTACCTGATAGATTTTCACTTTTCCATTCTGAATCA 1675 <u>AGAAGGCGTGTAAGACAGTTACGTGACTATGTCAATGTCAATTCAGATTGGTTATGTTAT</u> Conservative 0; Mismatches 195; 0 1755 1975 2155 1695 1815 1515 1275 1575 0

OCLI30W
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VOLI30W
SCYOLL30W
4202 bp DNA linear PLN 05-AUG-1997
ZINITION S.cerevisiae chromosome XV reading frame ORF YOLl30w.
ZESSION Z74872 Y13140
Z74872 1 GI:1420016
Z74872.1 GI:1420016

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Submitted (04-JUL-1996) Data collected by MIPS on behalf of the Suropean yeast chromosome XV sequencing project. MIPS at the Max-Planck-Institut fuer Biochemie, Am Klopferspitz 18a D-82152 Martinsried, FRG; E-mail: Mewes@mips.embnet.org
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Saccharomyces cerevisiae
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes; Saccharomycetales; Saccharomycetaceae; Saccharomyces.
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                                                                                                                             GATTTATTTAGAAAATGGTGAAGAAACTTGGTGGTTGGTAGATTGTACTTGTCCTACTGATTCG 1795
                                                                                                                                                                                                  GAAGAAACTATTCATGCCCCCGATATTCCATCATTAGTATCACCAGGTCAATCTGTTCGA
                                                                                                                                                                                                                                                                     TCTGATGGGATTAATGGAGGTTCATTACCTGATAGATTTTCACTTTTTCCATTCTGAATCA
 ATGCAAGAAACTCGTGAAAAAGTTGAATTATTTAAAAGTTATTATTTTTGTTTTCCAT 1915
                                                                                                       GAATTATTCAGGGGAGGTGAGCCAACATGGTGGTTAGATTGTAGTTGTCCAACTGATGAT 2437
                                                                                                                                                                          GATGAAACCGTTCATGCTAGTGATATCCCTTCCTTAGTGTCTGAGGGACAAACATTCTAT
                                                                                                                                                                                                                                             TCTTACCAGGGTACAGACTTTCAAATTCCTAATAGATTTTCTTTTTTTCTGTTCCGAATCT
                                  GAAATGAAAATGTTGGCCAAAGCATTTGGTATTCATCCTTTAACTGCTGAAGATATTCGA 1855
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ENENIPSNDPAYCSYQTDEQIPNRFSFFCSESDETVHASDIPSLVSEGQTPYELFFE
GEPTIMILDCSCCPTDDENRCIAKAFGHPLTAEDIRMQETREKVELFKSYYFVCFHTFE
NDKESEDPLEPINVYIVVCRSGVLTFHFGFISHCANVRRRVRQLRDYVNVNSDMLCYA
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/note="ARS-consensus"
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ASSGNKSKLSASSSASPITKVRKSSLVSPVLEIPHESKSDTHSKLAKPKKRTYSTTSA
HSSINPAVLLTKSTSQKSDADDTLERKPVRMNTRASFDSDVSQASRDSQETEEDVCF
PMPPQLHTRVNGIDFDELEEYAQFANAEKSQFLASLQVPNEQKYSNVSQDIGFTSSTS
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KADVIKMFAKRCQDEANGIGFALTSQINIANLQARQDNASHIKNNSSTTVPNNYAPTT
SQPRGDIALYLGDIQDHLLTMFQNLLAYEKIFSRSHTNYLAQLQVESFNSNNKVTEML
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/db_xref="SGD:S0005490"
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/cranslacion="MSSSSSSESSPMLSRSNSLANTMVSMKTEDHTGLYDHRQHPDS
/cranslacion="MSSSSSSESSPMLSRSNSLANTMVSMKTEDHTGLYDHRQHPDS
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SCU41293
13421 bp DNA linear PLN 18-OCT-1996
Saccharomyces cerevisiae putative serine/threonine protein kinase
gene, putative ribosomal protein L25 gene, and malate dehydrogenase
                                                                                                                                                                                                                                                                                                                                                   Submitted (24-NOV-1995) Joaquin Arino, Bioquimica I
Molecular, Universitat Autonoma Barcelona, Facultat
Bellaterra, Cerdanyola, Barcelona 08193, Spain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Casamayor, A., Khalid, H., Balcells, L., Aldea, M., Casas, C., Herrero, E. and Arino, J.
Sequence analysis of a 13.4 kbp fragment from the left arm of chromosome XV reveals a malate dehydrogenase gene, a putative ser/Thr protein kinase, the ribosomal L25 gene and four new or reading frames
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97051588
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Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GCTGATGTTATCAAAATGTTTGCCAAAAGATGCCAAGATGAAGCTAAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CANAGAATTGGTGAAAGTAGGCGTAAGACAATGACGTTGATGAGACTTCTTAGTGGTAAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GCAGATGCAATCGAAGATTCTGTGTTCATGGCTCGTGACATGGATTTTTGCAGCAATGTTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GCTGATGCCATTGAAGATGCCGTTTTCACTGCTAGAGATACTGATTTTAGTAGTATGTTA 2215
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GCTTTAATCGATGACATTACTGATAGTTTCGCTCCTGTAATTCAATCTATTGAATATGAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GCCTTAATCGATGAAATTACCGATGGTTTTGCCCCCCGTGATTCATGGAATTGAATATGAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AGAAGAAGAGTTCGTCAATTGAGAGATTATGTCGATGTTAGTGCTGATTGGTTATGTTAT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (bases 1 to 13421)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (bases 1 to 13421)
                                                                                                                                                                                                                                                                                                                       Location/Qualifiers
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                                                                                                                                                                                                  /mol_type="genomic
/strain="FY1679"
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                                                          .2995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1013-1020 (1996)
                                                                                                                                                                                                                                       DNA"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /translation="MSSSSSSSSSSSYLSRSNSLANTMVSMKTEDHTGLYDHRQHPDS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      complement (4368. .5495)
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/note="phosphothreonine residues"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note="Mdh2p; discrepancy in t
previously published sequence"
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/db_xref="GI:1209713"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         complement (7803. .9074)
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/db_xref="GI:1209714"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /protein_id="AAC49463.1"
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                                                                                                                       ERNQMLPICVSQLKKNIDKGLEFVASRSASS*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note="putative intron of putative ribosomal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             join(6364. .6376,6791. .7206)
/codon_start=1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               'codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 'gene="MDH2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                 codon start=1
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                                                                    2096
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                                                                                                                                                                                                                                                                                  GTTTTCCATGATGGTATATTAACGTTCCATTTTTCACCAATTTCTCATCCAGCAAATGTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ATGCAAGAAACACGTGAAAAGGTGGAACTTTTCAAATCGTATTACTTCGTTTTGTTTCCAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ATGCAAGAAACTCGTGAAAAAGTTGAATTATTTAAAAGTTATTATTTTGTTTTGCAT 1915
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GAAATGAAAATGTTGGCCAAAGCATTTGGTATTCATCCTTTAACTGCTGAAGATATTCGA 1855
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GAATTATTCAGGGGAGGTGAGCCAACATGGTGGTTAGATTGTAGTTGTCCAACTGATGAT 1810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GATGAAACCGTTCATGCTAGTGATATCCCTTCCTTAGTGTCTGAGGGACAAACATTCTAT 1750
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                                                                       GCCTTAATCGATGAAATTACCGATGGTTTTGCCCCCGTGATTCATGGAATTGAATATGAA 2155
                                                                                                                             AGAAGGCGTGTAAGACAGTTACGTGACTATGTCAATGTCAATTCAGATTGGTTATGTTAT
                                                                                                                                                                                   AGAAGAAGAGTTCGTCAATTGAGAGATTATGTCGATGTTAGTGCTGATTGGTTATGTTAT 2095
                                                                                                                                                                                                                                              GTCTGTAGGTCAGGTGTTTTAACATTCCATTTTGGCCCAATATCTCATTGTGCTAATGTC
                                                                                                                                                                                                                                                                                                                                                             ACCTTTGAAAATGATAAAGAATCAGAGGATTTCCTGGAACCTATTAACGTTTACATTGTT
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SGC

TTCGCTCCTGTAATTCAATCTATTGAATATGAA

2170

2110

2035

1990

1930

2050

CDS

gene intron SgS

CDS

Sg

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complement (11472. . .12773)
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/protein_id="AAC49468.1"
/db_xref="GI:1209717"
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/db_xref="GI:1209718"
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TCTGATGGGATTAATGGAGGTTCATTACCTGATAGATTTTCACTTTTCCATTCTGAATCA 1675 Conservative 11.2**%**; 72.5**%**; 0; Mismatches Score 396; DB 8; Pred. No. 2.5e-46; Length 13421; Indels ٥, Gaps 0

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APCOMMENT
Sequence split into 7
Fragment Name
CR380951_0
CR380951_1
CR380951_2
CR380951_3
CR380951_4
CR380951_5
CR380951_6
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GTCATGACTTTAATGAGATTATTATCAGGTAAAGCTGATGTCATTAAAAATGTTTGCTAAA 2302
                                                                                                                                                                                                                                                                GATTTCCTAGAGCCAATCAATGTATATGTGGTTGTATTTAGATCAGGTGTTTTGACATTT
                                                                                                                                                                                                                                                                                           GATTATTTAGAACCGATAAATGTTTATATTGTTGTTTTCCATGATGGTATATTAACGTTC
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                            ATGGCAAGAGACTTGGATTTTGCTGCGATGTTACAAAGGATCGGTGAAAGTAGGCGCAAA
                                                                                                                                             TATGTCGATGTTAGTGCTGATTGGTTATGTTATGCCTTAATCGATGAAATTACCGATGGT
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                                                        ACTGCTAGAGATACTGATTTTAGTAGTATGTTACAAAGAATTGGTGAATCAAGAAGAAAA 2242
                                                                                      TTTGCTCCAGTTATTAGATCGATAGAGCTAGAAGCGGACTCAATTGAAGACTCCGTGTTT
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             /mol_type="genomic DNA"
/strain="AB972"
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sulfite reductase flavoprotein; mithochondrial DNA-directed RNA polymerase; 12KD heat shock protein; 9KD nucleoporine-interacting component; DNA polymerase epsilon suppressor 4; FAB1 protein; GTP-binding protein YPT1; MD1 protein precursor; MutS protein homolog 4; actin; bZIP protein binding to CRE motif; calcium/calmodulin-dependent protein kinase type I; cell division control protein 14; cell division control protein 14; cell division control protein CDC26; chromosome segregation protein SMC1; chromosome segregation protein SMC2; cytoplasmic phenylalanyl-tRNA synthetase bata chain; depressed growth-rate protien; dihydrolipoamide dehydrogenase precursor; glycogen synthase isoform 1; hexokinase A; histidinol phosphatase; mitochondrial ribosomal protein YMR-31 precursor; nuclear integrity protein 1; pheromone alpha factor receptor; phosphate system positive regulatory protein, phosphomannomutase; proteosome component PRE4; rRNA helicase; rase-related protein; transposon TYI-17 154.0KD hypothetical protein; transposon TYI-17 49.8KD hypothetical protein; transposon TYI-17 49.8KD hypothetical
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Submitted (23-MAY-1995) Yasufumi Murakami, Tsukuba Life Science Submitted (23-MAY-1995) Yasufumi Murakami, Tsukuba Life Science Center, RIKEN, Division of Human Genome Research; 3-1-1 Koyadai, Tsukuba, Ibaraki 305, Japan (E-mail:yasufumi@rtcsl:riken:go.jp, Tsukuba, Ibaraki 305, Japan (E-mail:yasufumi@rtcsl:riken:go.jp, Tel:81-298-36-9137)
Tel:81-298-36-9059, Fax:81-298-36-9137)
On or before May 14, 2001 this sequence version replaced gi:836814, gi:2004274, gi:1100783, gi:871938, gi:871933, gi:1122225,
                                                                                                                                                                                                                                                                                    D31600:Submitted (25-May-1994)
D44594-D44606:Submitted (28-Dec-1994)
Sequence updated (16-Jan-1998)
Sequence updated (28-Dec-1995) by: Yan
Sequence data v3.0.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Murakami,Y., Naitou,M., Hagiwara,H., Shibata,T., Sasanuma,S., Sasanuma,M., Tsuchiya,Y., Soeda,E., Yamazaki,M., Tashiro,H. and Eki,T. Analysis of the nucleotide sequence of chromosome
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D50617 D31600 D44594 D44595 D44596 D44597 D44598 D44599 D4460
D44601 D44602 D44603 D44604 D44605 D44606
D50617 1 GI:2804269
                                                                                                                                                          We have corrected 2 sequence errors within some CDSs. Therefore, have revised 3 CDSs (YFL042c,43c,31w). YFL043c were connected to YFL042c and eliminated. The length of YFL031w (HAC1) became more
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            gi:870817, gi:1122230, gi:893419, gi:871957, gi:870821, gi:1122231
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Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
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                                                                                                                               longer than previous version.
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                                                                                 Location/Qualifiers
organism="Saccharomyces cerevisiae"
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Yokoyama, K.,
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KEAYRFKLTWFLKRISNIFMLIPFLNFLCCIYVSRGMCLLLRTLYLGWILFMLVQGFQ
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                                                                                                                                                                                                                                   6426. .7565
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                                                                                                                                                                                                                                                                                          /translation="mivnnahiltlpipyhapsviltitcilirhthtdativytist
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cinalntyviplehrilttqpiytyanitkksplkspkhknilsennnt"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 4823.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        4685
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /translation="mkvsdrrkfekanfdefesalnnkndlyhcesitlfesiftevr
sfyedeksglikvvkfrtgamnrkrsfekivisymvgknvqkfltfvedefdfqggfi
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     complement(3322.
/note="YFL064C"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /proteīn_id="BAA09176.1"
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/tzanslation="MATTODEVSGAPIVRSLQKSTIRKYGYNLAPHMFLLLHVDELSI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note="YFL065C"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           complement (1437. .2615)
/note="YFL066C"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /translation="MESIILSIAIFIGVLLGTSVGAGSGSSISPDVDAGSGSRTSPDV
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RIGTGIGTGIGSRISTSIGSRISPDVGTSSGNRISTGVSTGISTTMNARVAVLITAAI
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/db_xref="GI:836692"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ECQAERQLYDAYFH"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /codon_start=1
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/db_xref="GI:836691"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RDGGLCYLLSRKNSWAARNRKGELPPIKEGCITEQVREFYGLESKKGKKGQHVGCCVC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /codon_start=1
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/db_xref="GI:836688"
                                                                                                                                              /codon_start=1
/protein_id="BAA09179.1"
/db_xref="GI:836693"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   4823. .5000
/note="X element"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SAPVTATALLEARR"
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db_xref="GI:836687"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         066. .5521
note="YFL063W"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             'note="
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             codon_start=1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     note="Y' element"
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                                                                                                                                                                               Query Match
Best Local :
                                                                                                                                                    Matches
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                                                                                          1625 ATTAATGGAGGTTCATTACCTGATAGATTTTCACTTTTCCATTCTGAATCAGAAGAAACT 1684
                                                                                                                                                    803;
                                                                                                                                                                                  Similarity
                                       AATACAGAATATCAAATTCCTAGTAGATTTTCGTTCTTCCGCTCTGAATCTGAAACT
                                                                                                                                                                                                                                                                                                                        /translation="MADLFAPAPEPSTELGRLRVLSKSAGIRVSPLILGGMSIGDAWS
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KFTTDYKKYDVGGGKSANYCGNHKRSLHVSVRDSLRKLQTDWIDILYVHMWDYMSSIE
EVMDSLHILVQQARSSIWVCLIRLPGLFLRQITTLNLMVKPLLASIKVNGTC"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              / TEATIBLE LOTE "WISERVKTIGLAQMLKGGVIMDVVTPEQATIAERAGACAVMALER I PADMRKGGQVCRMSD PRMI KE I MEAVS I PVMAKVRI GHFVEAQILEBLQVDYI DESE VLTPADMTHII EKHNEKVPFVCGAKOLGEALLRI INEGAMI RTKGEAGTGDVSEAVKH ITKI KABI QQYKENLKTESD PAKATELRVPVDLLKTTLSSEKLPVVNPAAGGVATPA DAALLMQLGCEGVFVOSGI FKSSDPEKLACA I VEATTHYDNPAKLLQVSSDLGDLMGG DISIOSINEAGGKNGARLSE I GW"
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kreitapvilhislrvatqysvaiirdgepamdlogevlyvtclihdiattdkomratko
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nvgsntdlihidtvsainegfprlhwlscfatvvdtensrkpmghtssigddfskkvi
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CEWFFSHFFYRVLSAKKSMRALSLNVELWPYIKEAQLSCSEESLA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   complement (14793. .15431)
/note="YFL056C"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           KFLKAIKKATDYVLADPVKAMKEYIDFKPQLNNDLSYKQYQRCYAYFSSSLYNVHRDM
KKVTGYGKRLAILPPDYVSNYTNEYLSMPEPEEVSDPLEAQRLMAIHQEKCRQEGTFK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /trānslation="mtvvigvlalqqafibhyrhubkcivbrdpybkklsvmtvkdk
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dpbhvqvlykldgkdnggqblivaakqknnilatsfhpbelabndirfhdmfirbevlk
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SIKLTPEQIKYLESIIPFDVGFPTNFIGDDPAVTKKASLLTAMSAQISFD"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  complement (14305. .14763)
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/db_xref="GI:836696"
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/db_xref="GI:836698"
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                                                                                                                                                                                                                                                                       note="YFL055W"
                                                                                                                                                                                                                                                                                                      7004. .18680
                                                                                                                                                                                                                                                                                                                                                                                                                                                 /proteIn_id="BAA09185.1"
/db_xref="GI:836699"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           codon start=
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                                                                                                                                                                            10.9%;
59.8%;
                                                                                                                                                                               Score 383; DB (
Pred. No. 7e-45
                                                                                                                                                    Mismatches
                                                                                                                                                                                                           DB 8;
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2765 AAAATCACCGAAATGTTTTCTAAAATTACTTTGATTGGGACAATGTTAGTTCCATTAAAT 2824
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GATGGTATATTAACGTTCCATTTTTCACCAATTTCTCATCCAGCAAATGTTAGAAGAAGA 2044
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GCTGATAAAGAATCTGAAGATTATTTAGAACCGATAAATGTTTATATTGTTGTTTTCCAT 1984
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ATGTTGGCCAAAGCATTTGGTATTCATCCTTTAACTGCTGAAGATATTCGAATGCAAGAA 1864
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AGAAATGGTGAAGAAACTTGGTGGTTAGATTGTACTTGTTCCTACTGATTCGGAAATGAAA 1804
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GGTGAATCAAGAAGAAAAGTCATGACTTTAATGAGATTATTATCAGGTAAAGCTGATGTC 2284
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GATGATATCACAGATAGTTTTGCTCCGGTTATTCAATCCATCGAGTATGAAGCTGATTCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GATGAAATTACCGATGGTTTTTGCCCCCCGTGATTCATGGAATTTGAATATGAAGCTGATGCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GTAAGACAATTACGTGACTATGTCAGTGTCAATTCAGATTGGTTATGCTTTAATC 34148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GTTCGTCAATTGAGAGATTATGTCGATGTTAGTGCTGATTGGTTATGTTATGCCTTAATC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TCAGGTGTCTTGACTTTTCATTTTGACCCAATATCACACTGTGCCAATGTAAGAAGACGT 34208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AATGATAAAGAATCGGAGAATTATCTTGAACCTATAAATGTTTACATCGTTGTTTTTAGG 3426
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ACTCGTGAAAAAGTTGAATTATTTAAAAGTTATTATTATTTTGTTTTCCATACTTTTTGAA 1924
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AACAAATCTTTCCCCCATCCCCGATGCACGTCCAAGAGCTGATATTTGCATTATATTTTAGGT 2644
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GGAGTAGGAGTAGGAGGAATTAATTTTGGTCCCAATCCAACTGGAAATAATACTAATACT 2524
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ATTACTTCACCAATTAATTCAACTTTGAATCTTAATAGTTTAGGAACTTCAACTGGTGGA 2464
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ATTAAAATGTTTGCTAAAAGATGTCAAGAAGAAGCTAATTCTTCTTCTGGTTATTATCAA 2344
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ATTGAAGATGCCGTTTTCACTGCTAGAGATACTGATTTTAGTAGTATGTTACAAAGAATT 2224
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TGCATAGCAAAAAACATTTGGAATCCATCCTTTGACCGCGAAGATATCAGGATGCAAGAA 34388
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAGGGAGGCGATCCAACGTGGTGGTTGGATTGCAGTTGTCCAACTGATGATGAAATGCGT 34448
                                                        TCTAGATCACATGCAAACTACCTGGCCCAATTACAAGTGGAATCATTTAACTCTAATAAT
                                                                                                                                                                                                     GATATICAAGAICATAIAATCACCAIGIIICAAAAITTAITAGCCIAIGAAAAAATITIC 2704
                                                                                                                                                                                                                                                                                                                                                                                                                                                       AATACTAATACTACTGGTTCACCTTCACCACCTCAACAACAACAACAACATGGTATCACT 2584
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  59664 CCATACGTTCGAAAATGATATGGAATCGGAGGACTTTTTAGAGCCCATTAACGTCTATAT 5960
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                                      CCATACTTTTGAAGCTGATAAAGAATCTGAAGATTATTTAGAACCGATAAATGTTTATAT 1971
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                                                                   TTTTGGAATCCATCCCTTGACTGCCGAAGATATTCGGATGCAAGAGCCACGGGAAAAAGT
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Mammalia; Eutheria;
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Similarity 70.0%;
GATGAAATTACCGATGGTTTTGCCCCCGTGATTCATGGAATTGAAGATATGAAGCTGATGCC
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AGATTATGTCGATGTTAGTGCTGATTGGTTATGCTTATGCCTTAATCGATGAAATTACCGA
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CQ446161 684 bp DNA Sequence 11921 from Patent WO0192523. CQ446161 CQ446161.1 GI:41417311 Human polynucleotides and polypeptides Patent: WO 0192523-A 11921 06-DEC-2001; Curagen Corporation (US) Location/Qualifiers Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo. encoded linear thereby PAT 30-JAN-2004

1865 ACTCGTGAAAAAGTTGAATTATTTAAAAGTTATTTTTGTTTTGTTTTCCATACTTTTTGAA 1924 GCTGATAAAGAATCTGAAGATTATTTAGAACCGATAAATGTTTATATTGTTGTTTTCCAT 1984 GTTCGTCAATTGAGAGATTATGTCGATGTTAGTGCTGATTGGTTATGCCTTAATC TCAGGTGTCTTGACTTTTTGACCCAATATCACACTGTGCCAATGTAAGAAGACGT GATGGTATATTAACGTTCCATTTTTCACCAATTTCCCAGCCAAATGTTAGAAGAAGA 2044 **AATGATAAAGAATCGGAGAATTATCTTGAACCTATAAATGTTTACATCGTTGTTTTTAGG** <u>ACGCGTGAAAAGGTAGAGCTTTTCAAATCCTATTACTTTGTCTGTTTCCATACATTTGAA</u> Score 263.8; DB 6; Pred. No. 1.8e-27; 0; Mismatches 152; Indels Length <u>.</u> Gaps 180 2164 2104 120 60 240

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                                                                                                                                                                                                                                                                                                                                                                                                                                                            Churcher, C., Colling, M., Connor, R., Cronin, A., Davis, P., Churcher, C., Colling, M., Connor, R., Cronin, A., Davis, P., Feltwell, T., Fraser, A., Gentles, S., Goble, A., Hamlin, N., Harris, D., Hidalgo, J., Hodgson, G., Holroyd, S., Hornsby, T., Howarth, S., Huckle, B.J., Hunt, S., Jagels, K., James, K., Jones, L., Jones, M., Leather, S., McDonald, S., McLean, J., Mooney, P., Moule, S., McLeather, S., McDonald, S., McLean, J., Mooney, P., Moule, S., Murgall, K., Murphy, L., Niblett, D., Odell, C., Oliver, K., O'Neil, S., Pearson, D., Quail, M.A., Rabbinowitsch, E., Rutherford, K., Watter, S., Saunders, D., Quail, M.A., Rabbinowitsch, E., Rutherford, K., Rutter, S., Squares, R., Squares, S., Stevens, K., Taylor, K., Taylor, R.G., Tivey, A., Walsh, S., Warren, T., Whitchead, S., Woodward, J., Volckaert, G., Aert, R., Robben, J., Grymonprez, B., Weltjens, I., Vonctreels, B., Rieger, M., Schafer, M., Muller-Auer, S., Gabel, C., Puchs, M., Dusterhoft, A., Fritzc, C., Holzer, E., Moestl, D., Hilbert, H., Borzym, K., Langer, I., Beck, A., Lehrach, H., Reinhardt, R., Pohl T. M., Eger, P., Zimmermann, W., Wedler, H., Reinhardt, R., Pohl T. M., Eger, P., Galleu, E., Dreano, S., Hunt, C., Moore, K., Hurst, S.M., Lucas, M., Rochet, M., Gaillardin, C., Tallada, V.A., Garzon, A., Thode, G., Daga, R.R., Cruzado, L., Jimenez, J., Sanchez, M., Paulsen, I., Porsburg, S.L., Cerutti, L., Lowe, T., McComble, W. R., Paulsen, I., Potashkin, J., Shbakovski, G. V..
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                                                                                                                                                                                                                                                                                                                                                Lowe, T., McCombie, W.R., Paulsen, I., Potashkin, J., Shpakovski, G.V., Ussery, D., Barrell, B.G. and Nurse, P.
The genome sequence of Schizosaccharomyces pombe
Nature 415 (6874), 871-880 (2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ś
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes; Schizosaccharomycetales; Schizosaccharomycetaceae;
                                                                               Submitted (05-DEC-1997) European Schizosaccharomyces genome sequencing project, Sanger Institute, The Wellcome Trust Genome Campus, Hinxton, Cambridge CB10 1SA, E-mail: pombe@sanger.ac.uk QIAGEN GmbH, Max-Volmer-Str 4, D-40724 Hilden, Germany
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Stewart, A., Sgouros, J., Peat, N., Hayles, J., Baker, S., Bashar
Bowman, S., Brooks, K., Brown, D., Brown, S., Chillingworth, T.,
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Details of S. pombe sequencing at the Sanger Institute are available on the World Wide Web.
                                                       QIAGEN GmbH,
Notes:
                                                                                                                                                                                                                                                Wood, V., Rajandream, M.A., Barrell, B.G., Lauber, J., Hilbert, H. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GATGATATCACAGATAGTTTTGCTCCGGTTATTCAATCCATCGAGTATGAAGCTGATTCG
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A., Sgouros,J., Peat,N., Hayles,J., Baker,S., l
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         conflict
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since the original submission, therefore the complementary strand notation may be invalid for strand inference. IMPORTANT: This sequence WAY NOT be the entire insert of the sequenced clone. It
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           http://www.sanger.ac.uk/Projects/S_pombe/)
http://www.sanger.ac.uk/Projects/S_pombe/)
CDS are numbered using the following system eg SPAC5H10.01c. SP (S. pombe), A (chromosome 1), c5H10 (cosmid name), .01 (first CDS), c (complementary strand). However, clones may have been reprientated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         http://www.genedb.org/genedb/pombe/index.jsp) (URL,
                                                                                                                                                                                                           /note="C-5 sterol desaturase (predicted); involved in ergosterol biosynthesis (predicted); similar to S. cerevisiae ERG3"
                                                                                                                                                                                                                                                                                                complement (2261. .3250)
/gene="SPBC27B12.03c"
complement (2261. .3250)
/gene="SPBC27B12.03c"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note="ctaacatttgtcctag, splice branch complement (140. .145) /gene="SPBC27B12.01c"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /db_xref="UniProt/Trembl:042994"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         complement (82. .97)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note="synonym: SPBC30B4.09c"
complement(join(<1. .81,146.</pre>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         complement (join(1. .81,146. .886))
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                                                                                                                                                                                                                                                                                                                                                                                                                                  NVRAVKM"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TTLIVYSLYDSLHPSPGGLKHQVLNRITVIMIYFSPSNGAGQPAYMNLSFDPNFVI"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               consensus to allow contiguation"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SPAC30B4, we
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /protein_id="CAA16896.1"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                note="very hypothetical protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1526. .1855
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                note="synonym: SPBC30B4.10"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   gene="SPBC27B12.02"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    note="gtattc, splice"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            'gene="SPBC27B12.01c"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   gene="SPBC27B12.01c"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               'gene="SPBC27B12.01c"
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3.pombe chromosome 2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 clone="cosmid c27B12"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 'db_xref="taxon:4896"
'chromosome="II"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        db_xref="GI:2853108"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  citation=[2]
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           .pombe chromosome
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                                                                                                                                                                                    start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Τs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           in SPBC27B12 and SPAB4539, but only 11 in have altered c30B4 to agree with the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       donor sequence
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gene Sg

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misc_feature
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                                                                                                                                                                                                                                                                                                                                                              7278. .7376
/gene="SPBC27B12.05"
/note="Pfam match to e
G-bet a repeats"
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/note="gtacgc, splice dor
/note="gtacgc, splice dor
/note="spBC27B12.05"
/note="ctaattgtaattcag, splice dor
/note="ctaattgtaattcag, splices", splices
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ALKVLKLSVPFLGLKWKQANMSIITQIYLNCSLDIRDSMMFHENGSDTYKSAQLOETF
LAILIRFYHIRLYGKKCKSLYQFCILBEMRLKKSIEBLAASNMMEYIPESLWSYSFER
SDTGFFENEFAAMHINDIA
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FSDFLIYWIHRALHHRWLYAPLHKLHHKWIVPTPYSSHAFHYLDGYSQSLPYHWFPFF
FFLNKYVYLLLFGSVNYWTVLIHDGKYFSNNAVVNGAAHHAAHHMYFNYNYGQFFTLF
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7370...7382
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VQHSAMGLAVSPLRILGISSNSHNVNLFHLSPEFKRFXEDYHSPMFRQETLVLEGHEH
NIPCITFNSGGTLLLSGSIDRSLQIMDITSLSCLCKFYTKLRFIMGVKFIDKUAFYHI
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ALHRINMIECIPELQSVVCASQSGQLTLLRLICTTKILNGNPIYYVSFVPHKIRLTHL
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/note="additional C terminal exon to D1022301
WD repeat protein"
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AARNRKSNVKIBYTEDFATGFAISGEISHSINNLEFVLYSLSSLFLMMLKWFRLSHVL
RFERLAFLLYENHFLEIFNRHLTBGDCNRNTEKDVKCVRGGFFSYSSKMYKYDRVSIP
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SPENPSLLVNTAKTSKMSARRBQFQTNQNLPFCFTPNLEKLTIFYSVTEAANVFQNKT
KRTLAVBQLLSERELLRRFTLQQRLVADLHEFYNSVKGPAHSPETEDPVLKFVSQSYD
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/gene="SPBC27B12.04c"
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7507. .7512
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7825. .8253,8301. .8393)
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/note="PS00678 Beta-transducin
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CCCTACTGGTGAAATTGGTCTTTACCTTGGAGACATTCAAGACCA
                                  TTCTGGTTATTATCAACGTCAATATAACTTACAACAACAACAACA 2373
                                                                     TGGAAAGGCAGATGTTATTAAAATGCTCGCTAAGAGATGCAATGAAAAATGGACTATTGC
                                                                                                                                          TATGTTGAGACGAATTGGTGAATGTCGCAAAAAGACAATGGGAATGTTCCGACTTTTATA
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## SUMMARIES

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## ALIGNMENTS

06-MAR-2001 AAC87954; AAC87954 standard; DNA; 3525 BP (first entry)

Candida albicans CaALR1 nucleotide sequence

Candida albicans; yeast pathogen; identification; fungal; antifungal; CaKRE5; CaALR1; CaCDC24; diagnosis; fungicide; fungal infection; ds.

Candida albicans.

WO200068420-A2

16-NOV-2000.

05-MAY-2000; 2000WO-CA000533.

05-MAY-1999; 99US-0132878P.

(MYCO-) MYCOTA BIOSCIENCES INC.

Roemer T, Виввеу Н, Davison J;

P-PSDB; WPI; 2000-687652/67. AAB36515.

New DNA encoding essential proteins of Candida albicans, useful for diagnosing fungal infections and to screen for clinical or agricultural antifungal agents.

Claim 3; Fig 2A; 76pp; English

RESULT 1
AAC87926
AAC8926
AAC8926
ACC
AAC8
AA The present sequence represents the fungus-specific Candida albicans gene CaALRI. The present invention describes the fungus-specific genes CaKRES, CaALRI and CaCDC24 isolated in the yeast pathogen C. albicans. The genes have antifungal and fungicide activity. The genes in C. albicans and are useful as drug targets. Fragments of them are useful as probes and primers for diagnosis of fungal infections, also as antisense and ribozyme agents. Proteins encoded by the genes are used to screen for

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The invention relates to constructing (M1) a strain of diploid cells in which both alleles of a gene are modified, comprising one allele by insertion or replacement by a cassette having an

Claim

37;

SEQ ID NO 6675; 167pp + Sequence Listing;

English

modifying fungal expression.

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Constructing strains for identifying gene products as effective targets for therapeutic intervention, by inactivating in the strain one allele a gene and placing other allele of the gene under conditional expression

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22-AUG-2001; 2001US-0314050P.
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P-PSDB; ABP73838.
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CC expressible selectable marker and modifying other allele by recombination, of a promoter replacement fragment with a heterologous CC promoter, (an) is useful for constructing a strain of diploid fungal CC cells in which both alleles of a gene are modified. The diploid fungal CC cells having both alleles modified are useful for identifying a gene that CC is essential to the survival or growth of a fungus, a gene that CC contributes to the virulence and/or pathogenicity of a fungus, a gene that contributes to the resistance of a diploid fungus to an antifungal agent that inhibits the growth of a fungus and for identifying a therapeutic agent for treatment of a mammalian CC disease. (M1) is useful for identifying a compound which modulates the CC carpiulty of a gene product, preferably enzymatic activity, carbon CC compound catabolism, biosynthetic, transporter, transcriptional, CC cranslational, signal transduction, DNA replication and cell division CC activity. The method is useful for identifying a compound having the CC ability to inhibit growth or proliferation of C. albicans cells and for treating infection by C. albicans. The present sequence is that of an CC essential Candida albicans gene used in the method of the invention. CC specification but is based on sequence information supplied to Derwent by the European Patent Office
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Human; open reading frame; ORFX; gene therapy; cancer; cirrhosis; hyperproliferative disorder; psoriasis; benign tumour; haemorrhage; degenerative disorder; osteoarthritis; neurodegenerative disorder; cardiovascular disease; diabetes mellitus; systemic lupus erythematosus; hypertension; hypothyroidism; cholesterol ester storage disease; immune deficiency; immune disorder; infectious disease; autoimmune disorder; rheumatoid arthritis; autoimmune thyroiditis;
                                                                                                                                                                                                                                                                               The present invention describes substantially purified human proteins (referred to as open reading frame, ORFX where X is 1-11491 (see Tabin the specification). ABN15762 to ABN177252 encode the human ORFX proteins given in ABP00010 to ABP11500. ORFX proteins are useful for
                                                                                                                                                                                                                                                                                                                                                                     Novel human polypeptides and polynucleotides useful for diagnosing, preventing and treating cardiovascular disease, neurodegenerative, hyperproliferative disorders and autoimmune disorders.
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                                                                                                                                                                                                                                                                                                                                               Disclosure; SEQ ID NO 11921; 1037pp; English
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29-AUG-2000;
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2000US-0228716P.
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CC treating or preventing a patthology associated with an ORFX-associated CC disorder in humans, and in the manufacture of a medicament for treating a syndrome associated with ORFX-associated disorder. ORFX polynucleotide CC sequences can be used in gene therapy. ORFX sequences can be used in gene therapy. ORFX sequences can be used in the Creatment of cancer, hyperproliferative disorders, cirrhosis of liver, CC psoriasis, benign tumours, keloid, degenerative disorders, haemorrhage, CC osteoarthritis, neurodegenerative disorders, disorders related to organ CC transplantation, cardiovascular diseases, disorders related to organ CC lupus erythematosus, hypertension, hypothyroidism, cholesterol ester storage disease, various immune deficiencies and disorders, infectious CC diseases, autoimmune thyroiditis, myasthenia gravis, graft-versus-host CC diseases, autoimmune thyroiditis, myasthenia gravis, graft-versus-host CC diseases, autoimmune this flammatory eye disease. ORFX proteins are also CC useful for treating burns, incisions, ulcers, for treating osteoporosis, bone degenerative disorders, or periodontal disease, and for gut CC protection or regeneration and treatment of lung or liver fibrosis, CC reperfusion injury in various tissues and conditions resulting from CC systemic cytokine damage. N.B. The sequence data for this patent did not format directly from WIPO at ftp.wipo.int/pub/published\_pct\_sequences 684 BP; 223 A; 105 C; 140 G; 216 T; 0 U; 0 Other; see Table 1 ρ.

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Best Local Sin Matches 355; Query Match Similarity Conservative 7.5%; ; Score 263.8; ]; Pred. No. 1.2e 0; Mismatches .2e-36; DB 6; Length 684; Indels 0 Gaps 0

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ABT19393
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ID 1919393
ID 16-A
XX ABT1
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XX Pung
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27-APR-2001;
05-JUN-2001;
09-JUL-2001;
New purified or isolated nucleic acids of essential genes of Aspergillus fumigatus, useful for treating or preventing infections by A. fumigatus, or for treating a non-infectious disease in a subject e.g. cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Aspergillus fumigatus
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                                                                                    WPI; 2003-093124/08
                                                                                                                                                                                                                                                                                                                             23-APR-2002; 2002WO-US013142.
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cancer; contamination; biofilm; antibody; immune response; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Aspergillus fumigatus essential gene #1751.
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Disclosure; Page; 175pp; English

ce essential genes of Aspergillus funigatus. The isolated nucleic colds of the invention are used to treat or prevent infections by a pathogenic corganism such as A. funigatus, to treat a non-infectious disease in a consequence of the comparising A. funigatus to treat a non-infectious disease in a consequence of the pathogenic corganism such as A. funigatus. The polymucleotides are useful for comparising A. funigatus. The polymucleotides are useful for comparising comparising or combinant protein for characterisation, screening or corganisms invade or reside, for comparing with the DNA sequence of a corganisms invade or reside, for comparing with the DNA sequence of a corganisms invade or reside, for comparing with the DNA sequence of a corganisms to identify duplicated genes or paralogues having the same or similar biochemical activity and/or function, for comparing with DNA sequences of other related or distant pathogenic organisms to identify potential orthologous essential or virulence genes, for selecting and comparing or or anticomparing with DNA comparing organisms to identify sequences or organisms to identify the same or expression patterns, for raising anti-protein antibodies, as an corganism to a nucleic acid array for examination of expression patterns, for raising anti-protein antibodies, as an easy of identify inhibitors of the binding cours or to identify inhibitors of the binding cours or because of the protein organism invade or reside, and to isolate correlative receptors or ligands in the case or virulence consecution of the essential consecution of the invention of the essential genes of Aspergillus funigatus of the invention The invention relates to novel purified or isolated nucleic acids of

Sequence 1992 BP; 458 A; 509 C; 525 G; 500 T; 0 U; 0 Other;

Query Match Best Local : Local 1659 TTTTCCATTCTGAATCAGAAGAAACTATTCATGCCCCCGATATTCCATCATTAGTATCAC 959 similarity 56.6%; ATGTTAGTGCTGATTGGTTATGCCTTAATCGATGAAATTACCGATGGTTTTGCCC 2129 GTTATTATTTTGTTTGCATACTTT----TGAAGCTGATAAAGAATCTGAAGATTATT 1949 CAGGTCAATCTGTTCGAGATTTATTTAGAAATGG-----TGAAGAAACTTGGTGGTTAG CCGTGATTCATGGAATTGAAGCTGATGCCATTGAAGATGCCGTTTTCACTGCTA 2189 CCCTCAGTAGTGACTGGATCTGTTATGCCATGATTGACGACATTGTTGATAGTTTTTGGGC CACCAATTTCTCATCCAGCAAATGTTAGAAGAAGAGTTCGTCAATTGAGAGAGTTATGTCG 2069 TAGAACCGATAAATGTTTATATTGTTTGTTTTCCATGATGGTATATTAACGTTCCATTTTT 2009 CACTGACTACGGAAGATATCTTGACTCAAGAAGCCCGTGAAAAAGGTCGAGCTTTTCAAGC 1198 CTTTAACTGCTGAAGATATTCGAATGCAAGAAACTCGTGAAAAAGTTGAATTATTTAAAA 1892 ATTGTACTTGTCCTACTGATTCGGAAATGAAAATGTTGGCCAAAGCATTTGGTATTCATC 1832 TTTTCTCATCCGAGTCCCAGAGCACTGTGCATGCGGCGGAACTGGGGGGACCTTGTGCTCC CTGTCATCCGAGAGATTGAGATCGAATCTGAGGCAATTGAGGACCTCGTTTTCATCGCGC CCGAGAATCCACACGCGGCAAATGTCAGGAAGAGAATTGGGAAGCTTCGTGATTATGTGT 1378 TGGAGCCCGTCAACTTCTACATGGTTGTTTTCCGCGACGGTGTCCTCTCATTCTCATTCA Conservative Score 179.6; DB 8; Pred. No. 7e-22; 0; Mismatches 279; Length 1992; Indels 9; Gaps 1498 1438 1138 1078 1018 1718

GAGATACTGATTTTAGTAGTATGTTACAAAGAATTGGTGAATCAAGAAGAAAAGTCATGA

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therapeutic use, as markers for host tissues in which the pathogenic corganisms invade or reside, for comparing with the DNA sequence of A. Comparing the barrier of the similar biochemical activity and/or function, for comparing with DNA sequences of other related or distant pathogenic organisms to identify potential orthologous essential or virulence genes, for selecting and making oligomers for attachment to a nucleic acid array for examination of expression patterns, for raising anti-protein antibodies, as an antigen to raise anti-DNA antibodies or to elicit another immune response, and for identifying polynucleotides encoding the other protein with which binding occurs or to identify inhibitors of the binding cours of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The invention relates to novel purified or isolated nucleic acids of essential genes of Aspergillus fumigatus. The isolated nucleic acids of the invention are used to treat or prevent infections by a pathogenic organism such as A. fumigatus, to treat a non-infectious disease in a subject (e.g. cancer), to prevent or contain contannation of an object by A. fumigatus, or to prevent or inhibit formation on a surface of a biofilm comprising A. fumigatus. The polynucleotides are useful for expressing recombinant protein for characterisation, screening or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New purified or isolated nucleic acids of essential genes of Aspergillus fumigatus, useful for treating or preventing infections by A. fumigatus, or for treating a non-infectious disease in a subject e.g. cancer.
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27-APR-2001;
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09-JUL-2001;
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; 2001US-0287066P.
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RESULT 6
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Aspergillus oryzae; fermentation; expressed sequence tag; gene; ss.

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                                                                                                                                                                                                                                                     CCCTCACTAGTGACTGGATCTGTTATGCCATGATTGACGACATTGTTGATAGTTTTGGGC
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                                                                                       CTTTAATGAGATTATTATCAGGTAAAGCTGATGTCATTAAAATGTTTGCTAAAAGATGTC 2309
                                                                                                                         GCGTCGACGATTTTGAATCCTTCTTACCGCGAATCGGTGGCCTTCGTAAGAAGGTCATGA
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                                                                                                                                                                                        CTGTCATCCGAGAGATTGAGATCGAATCTGAGGCAATTGAGGACCTCGTTTTCATCGCGC 1498
                                                                                                                                                                                                                                                                                   ATGTTAGTGCTGATTGGTTATGTTATGCCTTAATCGATGAAATTACCGATGGTTTTGCCC
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                                                           GCTTGATGCGCCTTCTAGGTGGCAAAGCAGATGTCATTCGCGGTTTCTCCAAGCGTTGCA
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56.6%;
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Best Local Similarity 63.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The invention relates to a polynucleotide having any of 6006 specific sequences (ABZ50888-ABZ56893), which are expressed by a fungus under specific culture conditions including one or more of eutrophic, oligotrophic, solid, early germination, alkaline, high temperature, low temperature or maltose culture or polynucleotides stringently hybridising to these sequences. The polynucleotides are useful for monitoring the progress of fermentation and the growth conditions of a fungus, especially of Aspergillus oryzae which is widely used in industrial fermentation. Also monitoring for fungal contamination. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at form, but has obtained in electronic format directly from wipo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Detection of expression of specific Aspergillus genes for monitoring the fermentation and growth conditions of the fungus, using DNA probes.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Machida M,
Takeuchi M,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              at ftp.wipo.int/pub/published_pct_sequences
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                                                                                                                                                                                                                                                                                                                                                     CTTCGGGGTCCACGCGCTCACGGCAGAGGGATATCATGATGCAAGAGGCACGGGAGAAAGT
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TGTCTTCGGCCCGCTGATCCAGTCTATTGAGGATGAGGTCGACGAGATCGATG
                               TGGTTTTGCCCCCCGTGATTCATGGAATTGAATATGAAGCTGATGCCATTGAAG 2171
                                                                                                    AGATTATGTCGATGTTAGTGCTGATTGGTTATGTTATGCCTTAATCGATGAAATTACCGA 2118
                                                                                                                                                                           GTTCCATTTTTCACCAATTTCTCATCCAGCAAATGTTAGAAGAAGAGTTCGTCAATTGAG
                                                                                                                                                                                                              TGAGAACTATCTGCAACCAGTGAATATGTACGTGGTTGTGTTCCGGGAAGGAGTCTTGTC
                                                                                                                                                                                                                                                                                 TGAACTGTTTCGGAATTATTATTTTGTCAATTATCGGACCTTCGACCAAGACCCAAATAG
                                                                                                                                                                                                                                                                                                                TGAATTATTTAAAAGTTATTATTTTGTTTGTTTCCATACTTTTGAAGCTGATAAAGAATC
                                                                                                                                        CTTCCACTTTCTCAGACACCTCACCCGGCGAATGTGCGCCGGCGAATCCGTCAACTAAT
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Kobayashi
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RES INST BREWING.
FOOD RES INST MIN AGRIC.
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i T, Kitamoto N, Gomi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 169.4; DB 8; Pred. No. 3.7e-20;
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Abe K;
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RESULT

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ADRO1374/c
ID ADRO1374 standard; DNA; 537 BP
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AC ADRO1374;
XX
ADRO1374;
XX
Pilamentous funghi; ds; forens
KW Filamentous funghi; ds; forens
KW intergenomic comparison; chrom
XX
Eremothecium gossypii.
XX
29-MAY-2001.
XX
29-MAY-2001.
XX
21-DEC-1996; 97CH-00000016.
XX
31-DEC-1996; 97CH-00000016.
XX
AT 31-DEC-1996; 97CH-00000016.
XX
PI Philippsen P, Poehlmann R, &
PI Knechtle P, Rebischung C;
XX
PI Wew gene for adenylate Cyclase
PT generating recombinant microon
PT dependent signalling pathway i
XX
New gene for adenylate cyclase
PT genomic DNA sequences from the
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CC genomic DNA sequences for select
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Matches 2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The invention relates to isolated DNA molecules comprising isolated genomic DNA sequences from the filamentous funghi Ashbya gossypii, the sequences comprising ADR01309, ADR01366, ADR01367, ADR01388, ADR01468, ADR01637, ADR02057, ADR02345 and ADR02369, chosen from 1047 disclosed genomic sequences. Also included is a cloning vector comprising a nucleotide sequence chosen from the above sequences. The novel Ashbya gossypii genomic sequences are useful for forensic identification, gene characterisation, for studying gene organisation by intergenomic comparison (with Saccharomyces cerevisiae), identifying blosynthetic genes for selectable markers, to isolate promoters/terminators/centromeres, chromosome mapping, and in identifying sequences unique to Ashbya gossypii for species identification. The present sequence is an A. gossypii novel genomic sequence of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New gene for adenylate cyclase from Ashbya gossypii - useful for generating recombinant microorganisms with alteration in gene of cAMP-dependent signalling pathway for increasing production of fine chemicals.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Example 3; SEQ ID NO 66; 632pp; English.
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236; Conserv
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                                                                                                                                                                                                                                                                                                     CTCAACCAAGAGCTGATATAGCGCTCTATTTTGGGAGATATTCAGGACCATGTCCTCCCGA
                                                                                                                                                                                                                                                                                                                                       CACGTCCAAGAGCTGATATTGCATTATATTAGGTGATATTCAAGATCATATAATCACCA
                                  TTACTTTGATTGGGACAATGTTAGTTCCATTAAATTTAGTCACGGGACTTTTTTGGTATGA 2849
                                                                                                   CACAATTGCAAGTTGAGTCCTTCCGGTGTAACAATCGTGTTACTGAAATGTTGGGAAAGG 262
                                                                                                                                     CTCAATTACAAGTTGAATCATTCAATTCCAATAATAAAATCACCGAAATGTTTTCTAAAA 2789
                                                                                                                                                                                                       TGTTTCAAAATTTACTGTCCTATGAGAAGATTTTCTCCCCGTTCACATGGTAACTACTTGG
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     TCACTATGATTGGAACAATGTTAGTTCCTTTGAATCTTGTTACGGGTCTATTTGGGATGA
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Pred. No. 5.6e-20;
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CC Sequences ABP31028-ABP35561 represent 4534 novel human proteins CC designated ORF (open reading frame) 1-4534, and sequences ABN75054-CC ABN75587 represent cDNAs encoding them. The invention also encompasses CC DOLYPeptides at least 80% identical to the ORF1-ORF4534 (collectively referred to as ORFX) proteins, polynucleotides at least 85% identical to the ORFX nucleic acid sequences, vectors and host cells comprising ORFX CC polynucleotides, the recombinant production of ORFX proteins, antibodies specific for ORFX proteins, methods of detecting ORFX polynucleotides and collectivity, and methods of screening for modulators of ORFX expression or CC polypeptides, methods of screening for modulators of ORFX expression or CC contity, and methods of screening individuals for a predisposition to an CC polypeptides, methods of screening individuals for a predisposition to an CC contity, and methods of screening individuals for a predisposition to an CC contity, and methods of screening individuals for a predisposition to an CC contity, and methods of screening individuals for a predisposition, CC chemokinetia activities, such as cytokine, cell proliferation, CC chemokinetic activity, haemostatic activity, thrombolytic activity, chemotactic/c chemokinetic activity, haemostatic activity, thrombolytic activity, receptor/ligand, antiinflammatory activity, thrombolytic activity, crecaptor/ligand, antiinflammatory activity, thrombolytic activity, the determination
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Novel human polypeptides and polynucleotides useful for diagnosing, preventing and treating cardiovascular disease, neurodegenerative, hyperproliferative disorders and disorders related to organ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 24-MAY-2000; 2000US-0206690P
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       transplantation.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Page 829-830; 2508pp; English.
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Best Local
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                                                                                                                                                                                                                                                                       Human; haematopoietic cell proliferation disorder; cytostatic; gene therapy; lymphocytic leukaemia; acute myelogenous leukaem cytosine methylation state; gene; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            of bodily characteristics, fertility and behaviour. ORFX proteins, nucleic acids and antibodies may be used in the treatment of cancers, other proliferative disorders such as psoriasis and benign tumours, neurological disorders such as epilepsy and Alzheimer's disease, cardiovascular diseases, immune system disorders, disorders related to
Berlin K, Braun A, Distler J, Guetig D, Ho Olek A, Piepenbrock C, Adorjan P, Grabs G,
                                                                                                                                                                                                                                                                     gene therapy; lymphocytic leukaem; cytosine methylation state; gene;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 462 BP; 149 A; 83 C; 105 G; 125 T; 0 U; 0 Other;
                                                                                       26-MAR-2001; 2001US-0278333P
                                                                                                                          26-MAR-2002; 2002WO-EP003401.
                                                                                                                                                              03-OCT-2002
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                                                     (EPIG-) EPIGENOMICS
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Pred. No. 3.2e-11
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            biological sample obtained from the subject with at least 1 reagent, which distinguishes between methylated and non-methylated CpG dinucleotides within the target nucleic acid. ABZ09861 to ABZ1118 represent specifically claimed nucleotide sequences from the present invention. Oligonucleotides from the present invention can be used:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The present invention describes a method for detecting and differentiating between haematopoletic cell proliferative disorders associated with at least 1 gene and/or their regulatory regions in a subject. The method comprises contacting a target nucleic acid in a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Detecting and differentiating between hematopoietic cell proliferative disorders, comprises contacting a target nucleic acid with a reagent ti distinguishes between methylated and non-methylated CpG dinucleotides.
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                                                                              GAAAAAATCTAATCTTACCGATAAAGATAGAATTACCAACCCTATGAGTTTATCTGGTGG
                                                                                                                        TCAAGAGATTACATCAGATAATGCTAAACCATTGACTCGTAAATCTGGTTCTTCAATTAA
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standard; CDNA; 889 ВP

Aspergillus oryzae EST SEQ ID NO:7103

(first

entry)

Multiple gene expression; filamentous fungal cell; EST; expressed sequence tag; Fusarium venenatum, Aspergillus niger; Aspergillus oryzae; Trichoderma reesei; identification; recombination; culture condition; environmental stress; spore morphogenesis; metabolic pathway engineering; catabolic pathway engineering; ss. Aspergillus oryzae

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RESULT 11

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1659 TITTCCATTCTGAATCAGAAGAAACTATTCATGCCCCCCGATATTCCATCATTAGTATCAC 1718

Query Match Best Local

n 3.2%; Similarity 52.2%;

Score 113.6; DB Pred. No. 2.3e-10; Mismatches 2

2.3e-10; ches 279;

Indels 65; Length 2048; 0 Other;

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ABT20615

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                                                     The invention relates to novel purified or isolated nucleic acids of cc essential genes of Aspergillus fumigatus. The isolated nucleic acids of cc the invention are used to treat or prevent infections by a pathogenic cc organism such as A. fumigatus, to treat a non-infectious disease in a cc subject (e.g. cancer), to prevent or contain contamination of an object cc biofilm comprising A. fumigatus. The polynucleotides are useful for expressing recombinant protein for characterisation, screening or cc therapeutic use, as markers for host tissues in which the pathogenic cryanisms invade or reside, for comparing with the DNA sequence of A. cc fumigatus to identify duplicated genes or paralgues having the same or similar biochemical activity and/or function, for comparing with DNA sequences of other related or distant pathogenic organisms to identify potential orthologous essential or virulence genes, for selecting and cc making oligomers for attachment to a nucleic acid array for examination of expression patterns, for raising anti-protein antibodies, as an cc antigen to raise anti-DNA antibodies or to elicit another immune cresponse, and for identifying polynucleotides encoding the other protein with which binding occurs or to identify inhibitors of the binding ccurs or to identify inhibitors of the binding ccurs or to identify inhibitors of the binding ccurs of the protein in biological fluids, as a marker for host tissues in which pathogenic organism invade or reside, and to isolate correlative receptors or ligands in the case or virulence cc factors. This polynucleotide sequence represents one of the essential cc genes of Aspergillus fumigatus of the invention
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27-APR-2001; 2001US-0287066P.
05-UUN-2001; 2001US-0295890P.
09-UUL-2001; 2001US-0303899P.
31-AUG-2001; 2001US-0316362P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New purified or isolated nucleic acids of essential genes of Aspergillus fumigatus, useful for treating or preventing infections by A. fumigatus, or for treating a non-infectious disease in a subject e.g. cancer.
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cancer; contamination; biofilm; antibody; immune response; ds.
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                                                        Tishkoff D,
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                                                        Zamudio C,
                                                        Eroshkin AM,
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                                                        Lemieux
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New purified or isolated nucleic acids of essential genes of Aspergillus fumigatus, useful for treating or preventing infections by A. fumigatus, or for treating a non-infectious disease in a subject e.g. cancer.

English.

of expression patterns, for raising anti-protein antibodies, as an antiponse, and for identifying polynucleotides encoding the other protein with which binding occurs or to identify inhibitors of the binding interaction. The polypeptides may be used to raise antibodies or to elicit immune response, as a reagent in assays designed to quantitatively determine levels of the protein in biological fluids, as a marker for host tissues in which pathogenic organism invade or reside, and to isolate correlative receptors or ligands in the case or virulence factors. This polymucleotide sequence represents one of the essential genes of Aspergillus fumigatus of the invention biofilm comprising A. fumigatus. The polynucleotides are useful for expressing recombinant protein for characterisation, screening or therapeutic use, as markers for host tissues in which the pathogenic organisms invade or reside, for comparing with the DNA sequence of A. fumigatus to identify duplicated genes or paralogues having the same or similar biochemical activity and/or function, for comparing with DNA sequences of other related or distant pathogenic organisms to identify potential orthologous essential or virulence genes, for selecting and making oligomers for attachment to a nucleic acid array for examination The invention relates to novel purified or isolated nucleic acids of essential genes of Aspergillus funigatus. The isolated nucleic acids cessential genes used to treat or prevent infections by a pathogenic the invention are used to treat or prevent infectious disease in a organism such as A. fumigatus, to treat a non-infectious disease in a subject (e.g. cancer), to prevent or contain contamination of an by A. fumigatus, or to prevent or inhibit formation on a surface an object ace of a of.

밁 S 밁 S 밁 Ś 밁 Ş 밁 S 맑 S S Matches Query Match Local 1079 376; Similarity CACCAATTTCTCATCCAGCAAATGTTAGAAGAGAGAGTTCGTCAATTGAGAGATTATGTCG TAGAACCGATAAATGTTTATATTGTTGTTTTCCATGATGGTATATTAACGTTCCATTTTT GTTATTATTTTGTTTGCCATACTTT---TGAAGCTGATAAAGAATCTGAAGATTATT CTTTAACTGCTGAAGATATTCGAATGCAAGAAACTCGTGAAAAAGTTGAATTATTTAAAA 1892 ATTGTACTTGTCCTACTGATTCGGAAATGAAAATGTTGGCCAAAGCATTTGGTATTCATC CAGGTCAATCTGTTCGAGATTTATTTAGAAATGG-----TGAAGAAACTTGGTGGTTAG TTTTCTCATCCGAGTCCCAGAGCACTGTGCATGCGGGGAACTGGGGGGACCTTGTGCTCC TTTTCCATTCTGAATCAGAAGAAACTATTCATGCCCCCGATATTCCATCATTAGTATCAC 2048 BP; CCGAGAATCCACACGCGGCAAATGTCAGGAAGAGAATTGGGAAAGCTTCGTGATTATGTGT TGGAGCCCGTCAACTTCTACATGGTTGTTTTCCGCGACGGTGTCCTCTCATTCTCATTCA Conservative 473 3.2%; A; 520 C; 0, Score 113.6; DB 8 Pred. No. 2.3e-10; 0; Mismatches 279 540 G; 515 T; 0 U; 0 Other; DB 8; 279; Length 2048; Indels 65; Gaps 2069 1318 2009 1949 1138 1832 1078 1772 1018 ښ ۲۰

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RESULT 13
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The invention relates to novel purified or isolated nucleic acids of essential genes of Aspergillus fungatus. The isolated nucleic acids of the invention are used to treat or prevent infections by a pathogenic organism such as A. fumigatus, to treat a non-infectious disease in a subject (e.g. cancer), to prevent or contain contamination of an object by A. fumigatus, or to prevent or inhibit formation on a surface of a biofilm comprising A. fumigatus. The polynucleotides are useful for expressing recombinant protein for characterisation, screening or therapeutic use, as markers for host tissues in which the pathogenic organisms invade or reside, for comparing with the DNA sequence of A. fumigatus to identify duplicated genes or paralogues having the same or similar biochemical activity and/or function, for comparing with DNA
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27-APR-2001; 2001US-0287066P.
05-UUN-2001; 2001US-0295890P.
09-UUL-2001; 2001US-03103899P.
31-AUG-2001; 2001US-0316362P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New purified or isolated nucleic acids of essential genes of Aspergillus fumigatus, useful for treating or preventing infections by A. fumigatus, or for treating a non-infectious disease in a subject e.g. cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                              Disclosure; Page; 175pp; English.
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**ABT20019** 

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Similarity 52.2%;
76; Conservative
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                                                                                                            TACTGATTTTAGTAGTATGTTACAAAGAATTGGTGAATCAAGAAGAAAAGTCATGACTTT
                                                                                                                                                    TGAGACCGTCTAGTTCTAACGTTGGCACAGTGACGACATTGTTGATAGTTTTTGGGCCTGT
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                                    AATGAGATTATTATCAGGTAAAGCTGATGTCATTAAAATGTTTGCTAAAAGATGTCAAGA 2313
                                                                            CGACGATTTTGAATCCTTCTTACCGCGAATCGGTGGCCTTCGTAAGAAGGTCATGAGCTT
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Pred. No. 2.6e-10;
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Mismatches 279;
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                                                                                                                                                                                                                                                                     -GATGAAATTACCGATGGTTTTGCCCCCGT
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                                                                                                                                                                                                                                                                                                                CC therapeutic use, as markers for host tissues in which the pathogenic CC organisms invade or reside, for comparing with the DNA sequence of A. CC fumigatus to identify duplicated genes or paralogues having the same or CC similar blochemical activity and/or function, for comparing with DNA CC sequences of other related or distant pathogenic organisms to identify CC potential orthologous essential or virulence genes, for selecting and CC making oligomers for attachment to a nucleic acid array for examination CC expression patterns, for raising anti-protein antibodies, as an CC antigen to raise anti-DNA antibodies or to elicit another immune CC elicit immune response, and for identifying polymucleotides encoding the other protein comparing the binding CC interaction. The polypeptides may be used to raise antibodies or to celicit immune response, as a reagent in assays designed to quantitatively determine levels of the protein in biological fluids, as a marker for CC const tissues in which pathogenic organism invade or reside, and to isolate correlative receptors or ligands in the case or virulence CC factors. This polymucleotide sequence represents one of the essential CC genes of Aspergillus fumigatus of the invention
                                                                                                                                                                                                Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        subject (e.g. cancer), to prevent or contain contemination of an object by A. fumigatus, or to prevent or inhibit formation on a surface of a biofilm comprising A. fumigatus. The polynucleotides are useful for expressing recombinant protein for characterisation, screening or therapeutic use, as markers for host tissues in which the arrival or therapeutic use, as markers for host tissues in which the arrival or the surface of the surface 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The invention relates to novel purified or isolated nucleic acids of essential genes of Aspergillus fumigatus. The isolated nucleic acids the invention are used to treat or prevent infections by a pathogenic organism such as A. fumigatus, to treat a non-infectious disease in a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 23-APR-2001; 2001US-0285697P.
27-APR-2001; 2001US-0287066P.
05-UUN-2001; 2001US-029890P.
09-UUL-2001; 2001US-0303899P.
31-AUG-2001; 2001US-0316362P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Fungicide; cytostatic; essential gene; Aspergillus fumigatus; infection; cancer; contamination; biofilm; antibody; immune response; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Disclosure; Page; 175pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New purified or isolated nucleic acids of essential genes of Aspergillus fumigatus, useful for treating or preventing infections by A. fumigatus, or for treating a non-infectious disease in a subject e.g. cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Aspergillus fumigatus
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                                                                                                                                                                                                                                                               Sequence 4048 BP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 2003-093124/08
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Aspergillus fumigatus essential gene #2377.
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TTTTCTCATCCGAGTCCCAGAGCACTGTGCATGCGGCGGAACTGGGGGAACCTTGTGCTCC 2018
                                                           TTTTCCATTCTGAATCAGAAGAAACTATTCATGCCCCCGATATTCCATCATTAGTATCAC 1718
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                                                                                                                                                                                                                                                            925 A; 1043 C; 960 G; 1120 T; 0 U; 0 Other;
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                                                                                                                              Score 113.6; DB 8;
Pred. No. 2.6e-10;
D; Mismatches 279;
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                        (ELIT-)
                                                                                                                                                                                                                                                            Aspergillus
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                                                                                                                                                                                                                                                                                                                                               ADR84473 standard; DNA; 7990 BP
                                                                 17-JAN-2003; 2003US-0441281P
13-JUN-2003; 2003US-0478196P
                                                                                                        16-JAN-2004; 2004WO-US001099
                                                                                                                                     12-AUG-2004
                                                                                                                                                                                         Aspergillus fumigatus
                                                                                                                                                                                                                                  Fungicide; Aspergillus
                                                                                                                                                                                                                   screening;
                        ELITRA PHARM INC.
ELITRA CANADA LTD
                                                                                                                                                                                                                                                                                                                                                                                                                                              AATGAGATTATTATCAGGTAAAGCTGATGTCATTAAAATGTTTGCTAAAAGATGTCAAGA 2313
                                                                                                                                                                                                                                                                                                                                                                                                                    GATGCGCCTTCTAGGTGGCAAAGCAGATGTCATTCGCGGTTTCTCCAAGCGTTGCAACGA 2678
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TACTGATTTTAGTAGTATGTTACAAAGAATTGGTGAATCAAGAAGAAAAGTCATGACTTT 2253
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GATTCATGGAATTGAATATGAAGCTGATGCCATTGAAGATGCCGTTTTCACTGCTAGAGA 2193
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CCCTCAGTAGTGACTGGATCTGTTATGCCATGATGTAAGTCACAAGGGCGTGATTTCTAA 2438
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TAGAACCGATAAATGTTTATATTGTTGTTGTTTTCCATGATGGTATATTAACGTTCCATTTTT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CACTGACTACGGAAGATATCTTGACTCAAGAAGCCCGTGAAAAAGGTCGAGCTTTTCAAGC 2198
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CTTTAACTGCTGAAGATATTCGAATGCAAGAAACTCGTGAAAAAGTTGAATTATTTAAAA 1892
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ATTGTACTTGTCCTACTGATTCGGAAATGAAAATGTTGGCCAAAGCATTTGGTATTCATC 1832
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               fumigatus essential gene genomic sequence #284.
                                                                                                                                                                                                                                                                                         (first entry)
                                                                                                                                                                                                                     ds.
                                                                                                                                                                                                                                  fumigatus
                                                                                                                                                                                                                                  infection; Farmer's lung disease;
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Jiang B,

Hu W,

Lemieux S,

Roemer T;

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Query Match
Best Local Simi
Matches 376;
                                                                                 Claim 3; SEQ ID NO 284; 164pp; English.
                                                                                                          2004-594200/57.
DB; ADR86234.
    h 3.2%;
Similarity 52.2%;
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The present invention relates to Aspergillus fumigatus genes that are essential and are potential targets for drug screening. The methods and compositions of the present invention are useful for diagnosing and/or treating invesive Aspergillus fumigatus infection, including the allergic forms of the disease, such as Farmer's lung disease. They can also be found of the disease, such as Farmer's lung disease. They can also be used in various drug discovery purposes, such as expression of the recombinant protein, hybridization assay and construction of nucleic acid arrays. The present sequence represents an Aspergillus fumigatus essential gene full length genomic sequence, used during diagnosis and drug development in the invention. These genes share a high degree of sequence conservation with known essential genes of candida albicans. The sequence data for this patent is not represented in the printed New purified or isolated Aspergillus fumigatus nucleic acid molecule encoding a gene product, useful for diagnosing and/or treating invasive fungal infections, such as Farmer's lung disease. specification, but was obtained in electronic format from WIPO.

Sequence 7990 BP; 1925 A; 2042 C; 2031 G; 1992 T; 0 U; 0 Other; Score 113.6; DB 13; Length 7990; Pred. No. 2.9e-10; O; Mismatches 279; Indels 65;

밁 Ş 밁 문 ð 占 S 망 Ś 밁 밁 S 밁 망 1955 1895 2105 1835 1775 2010 1715 1950 1655 1893 1595 1833 1535 1719 1415 1659 ATGTTAGTGCTGATTGGTTATGTTATGCCTTAATC------TAGAACCGATAAATGTTTATATTGTTGTTTTCCATGATGGTATATTAACGTTCCATTTTT 2009 CAGGTCAATCTGTTCGAGATTTATTTAGAAATGG-----TGAAGAAACTTGGTGGTTAG CGACGATTTTGAATCCTTCTTACCGCGAATCGGTGGCCTTCGTAAGAAGGTCATGAGCTT TACTGATTTTAGTAGTATGTTACAAAGAATTGGTGAATCAAGAAGAAAAGTCATGACTTT GATTCATGGAATTGAAGCTGATGCCATTGAAGATGCCGTTTTCACTGCTAGAGA 2193 TGAGACCGTCTAGTTCTAACGTTGGCACAGTGACGACATTGTTGATAGTTTTGGGCCTGT -----GATGAAATTACCGATGGTTTTGCCCCCGT 2133 CCCTCAGTAGTGACTGGATCTGTTATGCCATGATGTAAGTCACAAGGGCGTGATTTCTAA 1894 CACCAATTTCTCATCCAGCAAATGTTAGAAGAAGAGAGTTCGTCAATTGAGAGAGTTATGTCG GTTATTATTTTGTTTGCTTTCCATACTTT---TGAAGCTGATAAAGAATCTGAAGATTATT 1949 CTTTAACTGCTGAAGATATTCGAATGCAAGAAACTCGTGAAAAAGTTGAATTATTTAAAA 1892 ATTGTACTTGTCCTACTGATTCGGAAATGAAAATGTTGGCCAAAGCATTTGGTATTCATC TTTTCTCATCCGAGTCCCAGAGCACTGTGCATGCGGCGGAACTGGGGGGACCTTGTGCTCC 1474 TTTTCCATTCTGAATCAGAAGAAACTATTCATGCCCCCGATATTCCATCATTAGTATCAC 1718 CCGAGAATCCACACGCGCAAATGTCAGGAAGAGAATTGGGAAGCTTCGTGATTATGTGT 1834 TGGAGCCCGTCAACTTCTACATGGTTGTTTTCCGCGACGGTGTCCTCTCATTCTCATTCA 1774 CACTGACTACGGAAGATATCTTGACTCAAGAAGCCCGTGAAAAGGTCGAGCTTTTCAAGC 1832 1772 2253 2014 1954 2069 1654 1594 1534 2104

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> 밁 S 2254 AATGAGATTATTATCAGGTAAAAGCTGATGTCATTAAAATGTTTGCTAAAAGATGTCAAGA 2313 2075 GÁTGCGCCTTCTÁGGTGGCÁÁÁGCAGÁTGTCÁTTCGCGGTTTCTCCAAGCGTTGCAACGA 2134

Search completed: April 14, Job time : 1755 secs 2005, 14:46:24

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Result
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Match Length DB
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3525
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1: /cgn2_6/ptodata/1/ina/5A_COMB.seq:*
2: /cgn2_6/ptodata/1/ina/5B_COMB.seq:*
3: /cgn2_6/ptodata/1/ina/6A_COMB.seq:*
4: /cgn2_6/ptodata/1/ina/6B_COMB.seq:*
5: /cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*
6: /cgn2_6/ptodata/1/ina/backfiles1.seq:*
   3.4 2445
2.1 708
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Copyright (c) 1993 - 2005 Compugen Ltd.
 US-09-248-796A-6328
US-08-984-16-6327
US-08-998-416-6302
US-09-248-796A-6302
US-09-248-796A-10622
US-09-248-796A-10622
US-09-949-016-12147
US-09-949-016-12423
US-09-949-016-12423
US-09-949-016-12699
US-09-949-016-15851
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Sequence 6328, Ap
Sequence 637, Appl
Sequence 66, Appl
Sequence 10622, Appl
Sequence 11, Appl
Sequence 12147, A
Sequence 17361, A
Sequence 17361, A
Sequence 16284, A
Sequence 16283, A
Sequence 12423, A
Sequence 12699, Appl
Sequence 11851, A
Sequence 15851, A
Sequence 15851, A
Sequence 15853, A
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Sequence 15853, A
Sequence 1724, A
Sequence 1725, A
Sequence 1725, A
Sequence 27, Appli
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B	RESULT US-09- Seq Feature Application of the FII FII FII FII FR. FR. FR. FR. FR. FR. FR. FR. FR. FR.	
345 ATAV 59 ATAV 405 TATV 119 TATV 465 AGTV 179 AGTV 179 AGTV 513 AACC 239 AACC	SSULT 1  S-09-248-796A-6328  Sequence 6328, Application US/ Patent No. 6747137  GENERAL INFORMATION: APPLICANT: Keith Weinstock et TITLE OF INVENTION: NUCLEIC A TITLE OF INVENTION: POR DIAG FILE REPERENCE: 107196.132 CURRENT FILING DATE: 1998-02-13 PRIOR APPLICATION NUMBER: US PRIOR FILING DATE: 1998-02-13 PRIOR FILING DATE: 1998-02-13 PRIOR FILING DATE: 1998-08-13 NUMBER OF SEQ ID NOS: 28208 SEQ ID NO 6328 LENGTH: 2358 TYPE: DNA ORGANISM: Candida albicans S-09-248-796A-6328 S-09-248-796A-6328 Gest Local Similarity 97.2%; Matches 2293; Conservative  y 285 ATAAATATAATTAAGAGGT  y 285 ATAAATATAATTAAGAGGT	63.4 63.4 61.2 61.2 61.2 60.6 60.6 60.6
GIGAAAGTTATT	",-6328 ",47137" RMATION: KEITH WEINSTOCK ET WENTION: NUCLEIC A VENTION: FOR DIAG NCE: 107196.132 LICATION NUMBER: U LICATION NUMBER: U LIGATE: 1999-02 CATION NUMBER: U G DATE: 1998-02-13 G DATE: 1998-02-13 G DATE: 1998-08-13 EQ ID NOS: 28208 58 58 CCANION SERVICE 18 198-08-198-08-198-08-198-08-198-08-198-08-198-08-198-08-198-08-198-08-198-08-198-08-198-198-198-198-198-198-198-198-198-19	1.8 187169 1.8 191569 1.8 114139 1.8 129415 1.8 147382 1.7 187169 1.7 19730 1.7 3095 1.7 1208 1.7 1208 1.7 1208 1.7 1208 1.7 451925 1.7 451925 1.7 451925 1.7 1039
ATCAAA  [        ATCAAA  GAAAATC          GAAAATC          GAAATC          CAGAAI          CAGAAI	US/092  C et al C ACID IAGNOS  1 18 60/ 13 18; 18 0; 18; 28; P 28; P 30; AGTATA	
ATAGTGAAAGTTATTATCAAAATTCAACTACTAATCAACCTATTCCTAGATCTAAAGIIIIIIIIII	AB796Å  AND AMINO ACID SEQUE TICS AND THERAPEUTICS 9/248,796A 074,725 096,409 096,409  CORE 2155.2; DB 4; red. No. 0; Mismatches 23; I TCTCCCCCTTTTGTTTTTTTTTTTTTTTTTTTTTTTTT	US-09-949-016-12776 US-09-949-016-15940 US-09-949-016-16997 US-09-949-016-12776 US-09-949-016-15940 US-09-949-016-15940 US-08-451-405A-2 5231168-1 5231168-1 US-09-949-016-379 US-09-949-016-12928 US-09-949-016-12928 US-09-949-016-12928 US-09-949-016-12928 US-09-949-016-12928 US-09-949-016-12928 US-09-949-016-12896 US-09-949-016-17305 US-09-949-016-17305 US-09-949-016-12896 US-09-949-016-12896 US-09-949-016-12896 US-09-949-016-12896 US-09-949-016-12896 US-09-949-016-12896 US-09-949-016-12896 US-09-949-016-12896 US-09-949-016-1280
CCTAGATCTGA	ENCES RELATING S Length 2358; Indels 44; TTCTTCCCAGCCAT	Sequence
	TO CANDIDA ALBICANS Gaps 8; GGTCCG 344 HILLI	12776, A 115940, A 115940, A 116997, A 14624, A 12776, A 15940, A 2, Appli 5231168 379, App 4309, Ap 12928, A 12928, A 12940, A 128740, A
	ALBICAN	

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1572 CTGGATCTGGATCTGGCAGGTGAAATTTGGTGGAGCAAGAATTTCTGATGGGATTAATG 1631	8 CACCTTACAAATATGATGATCAATTATCATTAACTTCATCTACATCTTCTACTT 	TTACTCATGAAAATTCTTCATCTTCAGAAGAAATTTATGAATTGAAGACTAAACAACAAC 151	TGGCAGCATTAAAATATACTCCCAAAAATATTTTTAAAGAAAACATTATCAAGATTTGAAT 145		ATGAATTTCAAAATCTTTCCAAAAATAATACTACTAGTGGTGCATCTCGTCATCCATATC 	AAGAAAGAGAAGAAGCTTATTTACAAAAACAAATGATTGCTAAAAAATATTCTGCGTATTG 12	TIGGIGATCATATIAGAGITAATIGAATITGATGAAATIGATGAATITATIAGAG 	1101 CTGATTCTCATGCATCAAGATCATCTCAAGAAACTGAAGAAGATGTTTGTT	CCACTGCTGCTGGTGGTGGTGGTAGAAGACCATCTCGTTCATCTATTGATAGTGAAG	90 AACTTTGGTATTTGGTGCTACAACCCTTGGTGTTTGGAACTTGGTACTTACCGCCACTTGCCACTTG	33 TGAAAACTAATGATAGTGAAGATATTACTAATACTAGCACCACTGCTAATCATATGA 98 	AATTIGGTOGTAATAATTCTAATAATTITGAAAATGATTTAGTTAGTCCCATGACAAAAA 93 	813 CTAATAAATCAAGAAGAAAATCTCAATTGGAAAATTTACCTCCATTAATAAAAAGAAAA 872 	753 ATCATACTCATCTTGCAATTCCAATTCCAATTCCAACCCCAATTATTACTAATG 812	TGAGTTCATTACGTAAAGATTTTTATTTAAAAGATAATACTGACGACAATTCTACTAATA	633 TGAGTTTATCTGGTGGTGATGATACTATTAACAGCGGTCACAAAAATCGTAATTATAACA 692 
RESULT 2 US-09-248-796A-6327 i Sequence 6327, Application US/09248796A  i Patent No. 6747137 i GENERAL INFORMATION: APPLICANT: Keith Weinstock et al i TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICANS i TITLE OF INVENTION: POR DIAGNOSTICS AND THERAPEUTICS  i FILE REFERENCE: 107196.132	Qy       2586 ACAAATCTTTCCCCATCCCC 2605	OY 2526 ATACTAATACTACTGGTTCACCTTCACCACCTCAACAACAACAACAACAGGTATCACTA 2585	OY 2466 GAGTAGGAGTAGGAGGAATTAATTTTGGTCCCAATCCAACTGGAAATAATAATACTAATACTA 2525	QY 2406 TTACTTCACCAATTAATTCAACTTTGAATCTTAATAGTTTAGGAACTTCAACTGGTGGAG 2465	Qy 2352 ATAACTTACAACAACAACAACAGGCCCCACCACCACCACCACCATCTATTA 2405	QY 2292 TGTTTGCTAAAAGATGTCAAGAAGAAGCTAATTCTTCTTCTGGTTATTATCAACGTCAAT 2351	OY 2232 CAAGAAGAAAAGTCATGACTTTAATGAGATTATTATCAGGTAAAGCTGATGTCATTAAAA 2291	OY 2172 ATGCCGTTTTCACTGCTAGAGATACTGATTTTAGTAGTATGTTACAAAGAATTTGGTGAAT 2231	OY 2112 TTACCGATGGTTTTGCCCCCGTGATTCATGGAATATGAAGCTGATGCCATTGAAG 2171	Qy 2052 AATTGAGAGATTATGTCGATGTTAGTGCTGATTGGTTATGCCTTAATCGATGAAA 2111	Qy 1992 TATTAACGTTCCATTTTTCACCAATTTCTCATCCAGCAAATGTTAGAAGAAGAGTTCGTC 2051	Qy 1932 AAGAATCTGAAGATTATTTAGAACCGATAAATGTTTATATTGTTGTTTTCCATGATGGTA 1991	OY 1872 AAAAAGTTGAATTATTTAAAAGTTATTATTTTGTTTGTT	1812 1559		Db 1439 CCCCCGATATTCCATCATTAGTATCACCAGGTCAATCTGTTCGAGATTTATTT

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PRIOR FILING DATE: 1998-08-13
NUMBER OF SEQ ID NOS: 28208
SEQ ID NO 6327
LENGTH: 507
                                                                                                                                                                                                                                                                                                                       Sequence 66, Application US/08998416 Patent No. 6239264
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Best Local Similarity
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CURRENT FILING DATE: 199-02-12
PRIOR APPLICATION NUMBER: US 60/074,725
PRIOR FILING DATE: 1998-02-13
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APPLICANT:
                                                                                                                                 APPLICANT: Rebischung, Corinne
TITLE OP INVENTION: GENOMIC DNA SEQUENCES OF ASHBYA GOSSYPII
TITLE OF INVENTION: AND USES THEREOF
NUMBER OF SEQUENCES: 1152
                                                                                                                                                                                                                                                                    APPLICANT:
                                                                                                                 CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                    APPLICANT:
COMPUTER READABLE FORM:
                                              STREET: 3054 Cornwallis Road
CITY: Research Triangle Park
STATE: No. 6239264th Carolina
                 COUNTRY: UZIP: 27709
                                                                                                 ADDRESSEE: No.
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ilarity 98.0%;
Conservative
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Knechtle, Philipp
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; Sequence 6302, Application US/09248796A ; Patent No. 6747137
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Best Local Similarity 67.6%;
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INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: CH 0016/S
PILING DATE: 31-DEC-1996
ATTORNEY/AGENT INFORMATION:
NAME: Meigs, J. Timothy
REGISTRATION NUMBER: 38,241
REFERENCE/DOCKET NUMBER: PF/5
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ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE CHARACTERISTICS:
LENGTH: 537 base pairs
TYPE: nucleic acid
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TELEPHONE: 919-541-8587
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
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Pred. No. 1.2e-25;
0; Mismatches 113;
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GENERAL INFORMATION:

APPLICANT: Keith Weinstock et al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING
TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 107196.132
CURRENT APPLICATION NUMBER: US/09/248,796A
CURRENT FILING DATE: 1999-02-12
PRIOR APPLICATION NUMBER: US 60/074,725
PRIOR APPLICATION NUMBER: US 60/096,409
PRIOR APPLICATION NUMBER: US 60/096,409

TO CANDIDA ALBICANS

FILING DATE: 1998-08-13

NOS:

28208

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; TYPE: DNA
; ORGANISM: Candida albicane
US-09-248-796A-6302
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                                                                                                                                                                                                                                                                                              ; TYPE: DNA
; ORGANISM: Candida albicans
US-09-248-796A-10622
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                                                                                                                                                                                                                                                                                                                                             PACENT NO. 6747137

GENERAL INFORMATION:

APPLICANT: Keith Weinstock et al
APPLICANT: Keith Weinstock et al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICAN
TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 107196.132
CURRENT APPLICATION NUMBER: US/09/248,796A
CURRENT FILING DATE: 1999-02-12
PRIOR APPLICATION NUMBER: US 60/074,725
PRIOR FILING DATE: 1998-02-13
PRIOR APPLICATION NUMBER: US 60/096,409
PRIOR FILING DATE: 1998-08-13
NUMBER OF SEQ ID NO 10622
LENGTH: 708
TYPE: NA
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SEQ ID NO 6302
LENGTH: 2445
                                                                                                                                                                                                                                          Query Match 2.1%;
Best Local Similarity 52.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 10622, Application US/09248796A
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
                                                                                                                                                                                                                       Matches 164;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2101 GAAATTGGAATGTATTTAGGTGATATACAAGATCATATTGTTACCATGTTGCAGGCCTTG
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                                  1250 CAAATGATTGCTAAAAATATTCTGCGTATTGATGAATTTCAAAATCTTTCCAAAAATAAT 1309
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GAATCATTCAATTCCAATAATAAAATCACCGAAATGTTTTCTAAAATTACTTTGATTGGG
                                                                                                          GATGATGATGACGATAGTAATATTAATATTGGTACTGTTAATGAAGATGATGAT
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GCAATGGATGCTGTGAATGATACAACTCGGAATAATAATCATAACAATAATAGAAATAGG
                                                                       GAATTGATTGATGATTATTTTCCAAGATGAATCAGATACACAAAGACAATTACGTCAA
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nilarity 60.4%;
Conservative
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Pred. No. 5.3e-15;
                                                                                                                                                                                                                                          Score 73.4; DB 4; Pred. No. 7.2e-06;
                                                                                                                                                                                                                         Mismatches 151;
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US-08-487-826B-13
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                                                                                                                                    Best Local Similarity Matches 290; Conserv
                                                                                                                                                                    Query Match
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CORRESPONDENCE ADDRESS:
ADDRESSEE: Knobbe Martens Olson & Bear
STREET: 620 Newport Center Drive 16th
CITY: Newport Beach
STRIE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Su, Xin-zigum.
APPLICANT: Wellems, Thomas E.
                                                                                                                                                                                                                                                                                                                                                                                                       NAME: ISTAELSEN, Ned
REGISTRATION NUMBER: 29,655
REFERENCE/DOCKET NUMBER: NII
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                     ANTI-SENSE: NO
                                                                                                                                                                                                                                   MOLECULE TYPE:
HYPOTHETICAL:
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                                                                                                                                                                                                                                                                                                        TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: US/0
FILING DATE: 10-SEP-1993
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                        TOPOLOGY:
                                                                                                                                                                                                                                                                                      STRANDEDNESS:
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                                                                                                                                                                                                                                                                                                                                                                                         TELEPHONE:
                                 2962 AAAATTGAATAATTCAATTGAAGGACAAAATAATGGTAATCGACCAATTTTTAATCATTC 3021
                                                                                                  2902 TGTTGGAGTATTAATATTTATAATTATTGGATCATTTATATTTGCTCAATGGTGGTTGAA
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                                                                                                                                    290; Conservative
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                                                                                                                                                                                                                                                                                                                                                                         (619) 235-8550
(619) 235-0176
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Miller, Louis H.
Peterson, David S.
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                                                                                                                                                                                                                                                                     linear
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                                                                                                                                                  2.0%;
46.8%;
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                                                                                                                                  Score 71.8; DB 2;
Pred. No. 5.1e-05;
0; Mismatches 328;
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   945
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RESULT 7
US-09-806-708B-22
                                                                                                                                                                                                                           ; NAME/KEY: promoter; LOCATION: (1)..(1141)
; COTHER INFORMATION: consensus sequence of A.t., L.a., US-09-806-708B-22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 22, Application US/09806708B
Patent NO. 6798342
GENERAL INFORMATION:
APPLICANT: The University of British Columbia
TITLE OF INVENTION: Regulation of Embryonic TI
FILE REFERENCE: 4810-58741
                                                                                                                                                                       Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                 SEQ ID NO 22
                                                                                                                                                        Matches
                                                                                                                                                                                                                                                                                                                                                                                               CURRENT APPLICATION NUMBER: US/09/806,708B CURRENT FILING DATE: 2001-04-03 PRIOR APPLICATION NUMBER: US 60/147,133 PRIOR FILING DATE: 1999-08-04 NUMBER OF SEQ ID NOS: 23 SOFTWARE: Patentin version 3.0
                                                                                                                                                                                                                                                                                                    LENGTH: 1141
TYPE: DNA
ORGANISM: Artificial sequence
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1425
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   119
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                                                                                                                                                                     h 2.0%; Score 68.8; DB 4; Similarity 11.6%; Pred. No. 7.8e-05;
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   GKTGWRHRYWRWRAMBDTVDHHYVTAMNNAWTTMCMMDKDDKRTRWWWKKNNNATGWDDD 178
                                     AATGATTGCTAAAAATATTCTGCGTATTGATGAATTTCAAAATCTTTCCAAAAATAATAATAC 1311
                                                                           WTWARMYCKYRRWYNNKSRWWKGWYKKKWYBCANNTSBRYHARRWKDMKTAYBMTWTNKW
                                                                                                                TAGTATATGTTATCAAAATATTATAATATGTAAATTATTAATAAAATATATTTGTATAAC
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                                                                                                                                                                                         Length 1141;
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US-09-949-016-12147
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GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
                                                           Sequence 12147, Application US/09949016 Patent No. 6812339
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1672
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                                                                                                                                                                           GKATCYMTDNAWW
                                                                                                                                                                                                             GTTACAAAGAATT 2224
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RESULT 9
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                                                                                                                  GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
                                                                                                                                                                                                                  Sequence 17361, Application US/09949016 Patent No. 6812339
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Best Local Similarity
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CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
                                                                                                           FILE REFERENCE: CL001307
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PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
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FILE REFERENCE: CL001307
CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
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ORGANISM: Human
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Pred. No. 0.0012;
0; Mismatches 240; Indels 0
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APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASS
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF
FILE REFERENCE: CL001307
CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR FILING DATE: 2000-10-23
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-09-08
PRIOR PRIOR DATE: 2000-09-08
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NAME/KEY: misc_feature

; LOCATION: (1)...(767677)

; OTHER INFORMATION: n = A,T,C

US-09-949-016-17361
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US-09-949-016-16284/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Patent No. 6812339
GENERAL INFORMATION:
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PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FAStSEQ for Windows Version
SEQ ID NO 17361.
LENGTH: 767677
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 16284, Application US/09949016
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Matches 212;
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Best Local Similarity 46.9%;
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ORGANISM: Human
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               343209 AGCCAAAGAAAACAAATATACTTTCAAACACAGAACTTTTTAGAATGCAATCCTTTTTAA
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OF DETECTION AND USES THEREOF
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APPLICANT: VENTER, J. Craig et al.
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASS
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF
FILE REFERENCE: CL001307
CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR FILING DATE: 2000-10-30
PRIOR APPLICATION NUMBER: 60/231,768
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR APPLICATION NUMBER: 50/231,498
PRIOR FILING DATE: 2000-09-08
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Patent No. 6812339
GENERAL INFORMATION:
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Best Local
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ORGANISM: Human
FEATURE:
NAME/KEY: misc_feature
LOCATION: (1)...(29717)
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NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FastSEQ for Windows Version
SEQ ID NO 12423
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Pred. No. 0.00044;
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                                                                                                                                                                                                                                   ASSOCIATED
OF DETECTION
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                                                                                                                                                                                                                                     DETECTION AND
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; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)...(60376)
; OTHER INFORMATION: n = 1
US-09-949-016-12423
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US-09-601-198-56/c
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                                        APPLICANT: Glass, Jennifer S.
APPLICANT: Glass, John I.
APPLICANT: Heiner, Cheryl R.
APPLICANT: Lefkowitz, Elliot
TITLE OF INVENTION: NUCLEIC ACID PROBES AND
TITLE OF INVENTION: UREALT/ICUM
FILE REFERENCE: UAB-13452/22
CURRENT FILING DATE: 2000-12-08
CURRENT FILING DATE: 2000-12-08
                                                                                                                                                                                                                                                                Sequence
                                                                                                                                                                                                                                  GENERAL INFORMATION:
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                                                                                                                                                                                                                                                    Patent No.
              PRIOR APPLICATION NUMBER: 60/073,189 PRIOR FILING DATE: 1998-01-30
                                                                                                                                                                               APPLICANT:
                                                                                                                                                                                               APPLICANT: Cassell, Gail H. APPLICANT: Chen, Ellson Y.
NUMBER OF SEQ ID NOS:
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TYPE: DNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2960 AAAAAATTGAATTAATTCAATTGAAGGACAAAATAATGGTAATCGACCAATTTTTAATCAT
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o. 6531583
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Pred. No. 0.00057;
0; Mismatches 295
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                                                                                                                  AND METHOD FOR DETECTING UREAPLASMA
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; LENGTH: 14066
; TYPE: DNA
; ORGANISM: Ureaplasma
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               TGTTTTCCTATGGTTGGTGATCATATTAGAGTTAATGGAATTGATTTTGATGAAATTGAT
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                                                                                                      AAATATAATGGACGTCAGATTAAAGTAGTTTATAAAGATAATAATAATGTTATCTATGAA
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                                             <u>AGTTCTTTAATTACATTACAAAAAAGGTAAAAATGACTATĆAATTATTGTTATCAAATTTA</u>
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Pred. No. 0.0005;
0; Mismatches 732; Indels 15;
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; TYPE: DNA
; ORGANISM: Human
US-09-949-016-12699
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Patent No. 6812339
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Best Local
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                                                                                                                                                                                                                                                                                 Local Similarity
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                                                                                                                                                                                                                                                                  tch 1.9%;
al Similarity 45.1%;
282; Conservative
                                                                                                                                                  ATTTATTTATATATATATTAATTTÄTATATAATTTAATTACATAATTATTTTTTATAATTA 1858;
                                                                                        ATTAGAAGTTTAGGTTTAAAAAAAACATGGTGGTAATAAATCAATTATTAGTTTCCCCAAT 3094
                              TATTTATAATTATTGGATCATTTATATTTGCTCAATGGTGGTTGAAAAAATTGAATAATT
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GTTAATTTTAAAGAAGAAACAACTTATAAATTAGTTAA 1925
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                                                                                                                                                                                                                                                              TGATTTGCTCCTAAAGAAACAATTAGAGATACTAATACATGGTTACAATACACAAGACCA
                                                                                                                                                                                                                                                                                                                         GGTGGTTCTAGTATGGCAGCATTAAAATATACTCCAAAAAATATTTTTAAAGAAAACATTA 1444
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                                                       TTGAAGACTAAACAACAACCACCTTACAAATATGATGA 1536
                                                                                                                           TTAAAAGATGTAACTAGTGATTTCAAAGAAGGAACTTGAGCGCATGATTTAAGTAATAGT 1963
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GENERAL INFORMATION:

APPLICANT: VENTER, J. Craig et al.

TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

FILE REFERENCE: CL001307

CURRENT APPLICATION NUMBER: US/09/949,016

CURRENT FILING DATE: 2000-04-14

PRIOR APPLICATION NUMBER: 60/241,755

PRIOR APPLICATION NUMBER: 60/237,768

PRIOR APPLICATION NUMBER: 60/237,768

PRIOR FILING DATE: 2000-10-03

PRIOR APPLICATION NUMBER: 60/231,498

PRIOR FILING DATE: 2000-09-08

NUMBER OF SEQ ID NOS: 207012

SOFTWARE: FastSEQ for Windows Version 4.0

LENGTH 10438 Application US/09949016 Score 66.4; DB 4; Pred. No. 0.00068; 0; Mismatches 342; Length 19438; Indels ۲. Gaps ۲

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RESULT 14
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CURRENT APPLICATION NUMBER: US/09/843,376
CURRENT FILING DATE: 2001-04-26
NUMBER OF SEQ ID NOS: 88
SEQ ID NO 10
LENGTH: 26000
TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 10, Application US/09843376 Patent No. 6566132
                                                                                                                                                                                                                                                                          Matches 225;
                                                                                                                                                                                                                                                                                      Query Match
Best Local
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Local Similarity 48.0%;
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                                   ATATTATTTACTATAAACATTTATTTTACGAGTTGTGTTAAATTGGAGAGTCAAATTAA
                                                                                 ATCATATTTATAATTGTATATAATCGTATACTAACTTCTTCTTGATTTAGGGAAAGAGTT
                                                                                                                                AGTTATTTCTATCAGTCAAAACAAA 19087
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                                                                                                                                                                                                                                                                                     Score 66; DB 4;
Pred. No. 0.00091;
                                                                                                                                                                                                                                                                                                DB 4; Length 26000;
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                                    TAATATATA 23856
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US-09-949-016-15851/c
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                                                                                                                                                                                                                                                                                                                                                                                 Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: DNA
ORGANISM: Human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ENGTH: 205044
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CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILLING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
PRIOR FILING DATE: 2000-09-08
PRIOR FILING DATE: 2000-09-08
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILE REFERENCE: CL00130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FEATURE:
NAME/KEY: misc_feature
LOCATION: (1)...(205044)
OTHER INFORMATION: n = A,T,C
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Local Similarity 44.3%;
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TCAATTCCAATAATAAAATCACCGAAATGTTTTCTAAAATTACTTTGATTGGGACAATGT
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                                                                                                                                                                                GATCATTTATATTTGCTCAATGGTGGTTGAAAAAATTGAATAATTCAATTGAAGGACAAA
                                                                                                                                     GTGGTACCAATTTAGGTTGGTTTTTCGGAATTGTTGGAGTATTAATATTTATAATTATTG
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                                           ACAGAAGGGGGGGAAGGAGAAGGGGATATATATCGGCATTTGTTGGTACTTTTGTTTTT 3474
                                                                                       ATAATGGTAATCGACCAATTTTTAATCATTCATCAAGAAGATCAATTAGAAGTTTAGGTT
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Pred. No. 0.0021;
0; Mismatches 392;
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